GenCore version 5.1.4_p5_4578
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OM nucleic - protein search, using frame_plus_n2p model

Run on: May 7, 2003, 15:14:59 ; Search time 200 Seconds
                  (without alignments)
                  6700.652 Million cell updates/sec

Title: US-09-965-830-1_COPY_6_3257
Perfect score: 6089
Sequence: 1 atgccggccatgcggggcct................aagaaggcacaggggtctga 3252

Scoring table: BLOSUM62
                  Xgapop   10.0 , Xgapext   0.5
                  Ygapop   10.0 , Ygapext   0.5
                  Fgapop   6.0 , Fgapext   7.0
                  Delop   6.0 , Delext   7.0

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1343160

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

Command line parameters:
-MODEL=frame_n2p.model -DEV=xlp
-O=/cgn2_1/USPTO_spool/US09965830/runat_07052003_151449_6257/app_query.fasta_1.3399
-DB=SPTREMBL_21 -QFMT=fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCI=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09965830.@CGN_1_1.350_@runat_07052003_151449_6257 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   SPTREMBL_21:*
                  1: sp_archea:*
                  2: sp_bacteria:*
                  3: sp_fungi:*
                  4: sp_human:*
                  5: sp_invertebrate:*
                  6: sp_mammal:*
                  7: sp_mhc:*
                  8: sp_organelle:*
                  9: sp_phage:*
                  10: sp_plant:*
                  11: sp_rodent:*
                  12: sp_virus:*
                  13: sp_vertebrate:*
                  14: sp_unclassified:*
                  15: sp_rvirus:*
                  16: sp_bacterial:*
                  17: sp_archeap:*

                                          SUMMARIES

Result   Query
NO.   Score   Match Length DB   ID   Description
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1   5704   93.7   1117   4   Q9ULD8   Q9uld8 homo sapien

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

RESULT 1
Q9ULD8

ID   Q9ULD8   PRELIMINARY;   PRT;   1117 AA.
AC   Q9ULD8; Q9UQ06;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   KIAA1282 protein (BEC1) (Fragment).
GN   KIAA1282.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=20039619; PubMed=10574462;
RA   Nagase T., Ishikawa K., Kikuno R., Hirosawa M., Nomura N., Ohara O.;
RT   "Prediction of the coding sequences of unidentified human genes. XV.
RT   The complete sequences of 100 new cDNA clones from brain which code
RT   for large proteins in vitro.";
RL   DNA Res. 6:337-345(1999).
RN   [2]
RP   SEQUENCE OF 35-1117 FROM N.A.
RC   TISSUE=BRAIN;

                                      ALIGNMENTS

2	5428	89.1	1087	11	O89047	O89047 rattus norv
3	5416	88.9	1087	11	Q9wvj0	Q9wvj0 mus musculu
4	2529.5	41.5	1107	4	O96L42	O96L42 homo sapien
5	2515	41.3	1102	11	O88877	O88877 rattus norv
6	2461.5	40.4	1017	4	Q9UQ05	Q9UQ05 homo sapien
7	2447.5	40.2	1017	11	Q9RI9	Q9RI9 rattus norv
8	2439.5	40.1	1017	11	Q9RI9	Q9RI9 rattus norv
9	1901	31.2	1284	5	Q23974	Q23974 drosophila
10	1901	31.2	1311	5	Q9V899	Q9V899 drosophila
11	1551	25.5	1158	6	Q9TS23	Q9TS23 canis famil
12	1547	25.4	1162	11	O35221	O35221 mus musculu
13	1543	25.3	1162	6	Q8WNY2	Q8WNY2 oryctolagus
14	1539	25.3	1163	11	O35219	O35219 mus musculu
15	1537.5	25.3	1163	4	O08962	O08962 homo sapien
16	1509.5	24.8	994	4	Q9H252	Q9H252 homo sapien
17	1499.5	24.6	1144	6	O19119	O19119 oryctolagus
18	1475	24.2	950	11	O54853	O54853 rattus norv
19	1400.5	23.0	1195	11	Q9ER47	Q9ER47 rattus norv
20	1399.5	22.9	1195	11	O54852	O54852 mus musculu
21	1387	22.8	1174	5	Q9VXZ6	Q9VXZ6 rattus norv
22	1384.5	22.7	1196	4	Q9NS40	Q9NS40 homo sapien
23	1380.5	22.7	962	11	Q63472	Q63472 rattus norv
24	1378	22.6	960	6	O18965	O18965 bos taurus
25	1371.5	22.5	989	11	O60603	O60603 mus musculu
26	1369	22.5	962	4	O76035	O76035 homo sapien
27	1367.5	22.5	987	6	O18966	O18966 bos taurus
28	1361	22.4	888	4	Q9H3P0	Q9H3P0 homo sapien
29	1358.5	22.3	989	11	O95259	O95259 homo sapien
30	1339.5	22.0	988	4	O95259	O95259 homo sapien
31	1337.5	22.0	988	11	Q9QXT2	Q9QXT2 rattus norv
32	1268.5	20.8	988	11	Q9EPI9	Q9EPI9 rattus norv
33	1261.5	20.7	820	11	O35989	O35989 mus musculu
34	1261.5	20.7	956	5	Q9XYX7	Q9XYX7 caenorhabdi
35	1259.5	20.7	956	5	O44164	O44164 caenorhabdi
36	1257.5	20.7	820	11	O35220	O35220 mus musculu
37	1232	20.2	366	11	O90WS8	Q9QWS8 rattus norv
38	1185.5	19.5	772	4	Q9BUT7	Q9BUT7 homo sapien
39	1084	17.8	791	5	O18325	O18325 caenorhabdi
40	1046	17.2	855	5	O02497	O02497 drosophila
41	1035.5	17.0	526	13	Q9PT84	Q9PT84 gallus gall
42	1035	17.0	502	4	Q9BRD7	Q9BRD7 homo sapien
43	938.5	15.4	1198	11	Q9JKA7	Q9JKA7 rattus norv
44	577	9.5	1203	6	Q9UMQ7	Q9UMQ7 homo sapien
45	566	9.3	1203	4	Q9Y3Q4	Q9Y3Q4 homo sapien
	566	9.3	1203	4	Q9y3q4	Q9y3q4 homo sapien
	562.5	9.2	1175	6	Q9TV66	Q9tv66 oryctolagus

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RX   MEDLINE; 99386988; PubMed=10455180;
RA   Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;
RT   "New ether-a-go-go K+ channel family members localized in human
RT   telencephalon.";
RL   J. Biol. Chem. 274:25018-25025(1999).
DR   EMBL; AB033108; BAA86596.1; -.
DR   EMBL; AB022696; BAA83590.1; -.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS_domain.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   PROSITE; PS50042; cNMP_BINDING_3; 1.
DR   TIGRFAMS; TIGR00229; sensory_box; 1.
DR   SMART; SM00091; PAS; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00100; CNMP; 1.
DR   Pfam; PF00785; PAC; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00027; cNMP_binding; 1.
FT   NON_TER       1      1
SQ   SEQUENCE   1117 AA;  120471 MW;  163A100B7141CA53 CRC64;
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Alignment Scores:

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Pred. No.:
Score:                 5.12e-309
Score:                 5704.00
Percent Similarity:    100.00%
Best Local Similarity: 100.00%
Query Match:           93.68%
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US-09-965-830-1_COPY_6_3257 (1-3252) x Q9ULD8 (1-1117)

Length:          1117
Matches:         1083
Conservative:       0
Mismatches:         0
Indels:             0
Gaps:               0
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Qy    1 ATGCGGCCAATGGCGGGGCGGCTCCTGGCGCTCAGAGACACCTTCCTTGACACCATGCTACG  60
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Db   35 MetProAlaMetArgGlyLeuLeuLeuAlaLeuArgAspThrPheLeuAspThrMetLeuAlaThr  54

Qy   61 CGCTTCGACGGCACGGCACAGTAACTTCGTCGTCGGCCAACGCCCCAGTGGCCGGGGCTCTTC 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   55 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnValAlaGlyLeuPhe  74

Qy  121 CCCGTGGTCTACTGCTCTGATGGGTCGTTCTTGTGACCTCACGGGCCTTCTCCCGGCGTGAGGTC 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   75 ProValValTyrCysSerAspGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal  94

Qy  181 ATGCAGCGGGGGCTGTGCCCGCTGCCTTCCTTTATGGGCCCAGACACCAGTGAGCTCGTCCGC 240
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   95 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluLeuValArg 114

Qy  241 CAACAGATACCGCAAGGCCCTGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  115 GlnGlnIleArgLysAlaLeuThrSerThrArgGluPheLysAlaGluLeuIleLeuTyr 134

Qy  301 CGGAAGAGACCGGGCTCCCGTTCTCGGTGTCTCGGATGTGATACCCATAAAAGAATGAGAA 360
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  135 ArgLysArgProHisSerProPheCysLeuLeuAspValIleProIleLysGluLys 154

Qy  361 GGGGAGGGTGGCCGTCTCTTCCTAGTCTCACAAGGACAATCCGAAACCAAGAACCGAGG 420
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  155 GlyGluValAlaLeuLeuPheLeuValSerHisLysAspIleSerGlyuThrLysAsnArgGly 174

Qy  421 GGCCCCGACGATGGAGGAGACAAGGTGGTGCGGGGGGGGGCCGGGACACGATCC 480
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Db  175 GlyProAspArgTrpLysGlyThrHisGlyGlyValArgArgArgTyrGlyArgAlaArgSer 194

Qy  481 AAAGGCTTCAATGCCACACCGGGGCGCGGCGGCCGGCGTGCTCTACCACCTGTCCGGGGCAC 540
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Db  195 LysGlyPheAsnAlaLeuAsnArgArgArgSerArgPheLeuTyrHisLeuSerGlyHis 214

Qy  541 CTGCAGAAGCAGCGCCCCAAGGGACAAGCACAGCTCAATAAGGGGGGTGTTTGGGGAGAAACCA 600
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Db  215 LeuGlnLysGlnProLysGlyLysHisLysLeuAsnLysGlyValProPheGlyGluLysPro 234

Qy  601 AACTTGCCTGAGTACAAAGTAGCCCCCATCCGGAAGTCGCCCTTCATCCTGTTGCACTGT 660
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Db  235 AsnLeuProGluTyrLysValAlaProIleArgLysSerProPheIleLeuLeuHisCys 254

Qy  661 GGGGCACTGAGCAGCCACACCTGGGATGGCCCCATCCGGCACACTCTATGTGGCCTGTC 720
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Db  255 GlyAlaLeuSerSerHisThrTrpAspGlyProIleArgHisThrLeuCysGlyLeuSer 274

Qy  721 ACTGTGCCCTACACAGGGTGTGTGTGAGCACACGACCAGGGAGCCCCAGTGCCGGCCG 780
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Db  275 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 294

Qy  781 CCCAGCGGTCTCTGACCTGGCCGTGGGAGGTCCTTCTTCATCCTTGACATTGTTGCTGAATTTC 840
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Db  295 ProSerValCysSerAspLeuAlaValGluValLeuPheLeuLeuLeuAspIleLeuAsnPhe 314

Qy  841 CGTACCACATTCGTTGTTCCAAGTCCCCAGGTTGGTTTGTGTTTGGCCCCAAAGTCCAATTTTGCCTC 900
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Db  315 ArgThrThrPheValSerLysSerGlnValValValProArgLeuGlySerIleCysSerLeu 334

Qy  901 CACTACGTCACCACCTGGTTCCTGCTGGTTCCGCGGGGCCTGCGGCCCGTACTCGCAGTACGGGGGCTGCTA 960
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Db  335 HisTyrValThrThrTrpPheLeuLeuValProArgGlyLeuArgProValLeuAlaValAlaValLeu 354

Qy  961 CATGGCCTTCAAGGTCAACGTGTTCTCGCCCTGCTCTCGCCGCGACTGGGGTCGCGGGTGGGGCCCTGCTG 1020
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Db  355 HisAlaPheLysValAsnValPheSerGlyAlaHisIleLeuLeuAspTrpValAlaCysValThrTrpPheTyr 374

Qy 1021 CGCCTGCTTGCGCCTGCCTGTTCCTGCGTGGCGGGCTGCGGACCGGTACTGCCAGTACACGCCGGGTGCTG 1080
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  375 ArgLeuLeuArgLeuLeuProAlaCysLeuAspAlaArgThrArgThrArgTyrArgSerArgAlaValLeu 394

Qy 1081 ACACTGCTCATGCCGTGTTCGCCCTGCTCTCGCCGCGACTGGGGTCGCGGGTGGGGCCCTGCTTAC 1140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  395 ThrLeuLeuMetAlaValAlaValPheAlaLeuLeuAlaHisTrpValAlaCysValThrTrpPheTyr 414

Qy 1141 ATTGGCCAGCGGGGAGATCGAGAGCGACCAGCCAGAATCCGAGCGTCCCTGAGATTGGCTGCAG 1200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  415 IleGlyLeuArgGluIleGluSerGluGluSerGluLeuProGluIleLeuProGluLeuGln 434

Qy 1201 GAGCTGGGCCCCGGGCGGCCGGCCGGGGCCGTCGTCGCCGCCCGCGGCGGCCGGGGCCGGAGG 1260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  435 GluLeuAlaLysArgLeuGluThrProTyrArgGlyGlyArgArgProAlaGlyGly 454

Qy 1261 AACAGCTCCGGCCAGAGTGACAACTGCAGCAGCAGCAGGAGGCCAACGGGACGGGCTG 1320
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  455 AsnSerSerGlyGlnSerAspAsnCysSerSerSerSerGluAlaAsnGlyThrGlyLeu 474

Qy 1321 GAGCTGCTGGGGCGGGGGCGGCGCGTCGCTGCGCCAGCCGCCTACATCACCTTCTACTTCCCACTC 1380
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Db  475 GluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuThrProThrAlaLeu 494

Qy 1381 AGCAGCCTCACCAGCGGTGGGCTTCGGCAAGGTGTCGCCAACAGGGACCCGAGAGATC 1440
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  495 SerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThrGluLysIle 514

Qy 1441 TTCTCCAATGCCACCATGCTCATACGGCGCCGCTGATCGACACCGCGTGTGTTTGGGAACGTG 1500
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  515 PheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValAlaPheGlyAsnVal 534

Qy 1501 ACGGCCATCACCCAGCGACAGTACCGCCGGCGCTTTGTGACCCACAGCGCCACGCGCGAC 1560
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Db  535 ThrAlaIleIleGlnArgMetTyrAlaAlaArgPheLeuTyrHisSerArgThrArgAsp 554

Qy 1561 CTGCGCGACTACACATCCGCCATCCACCCGTTATCCCCAGCCCTCAAGCGGCCAATGCCTGGAG 1620
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  555 LeuArgAspTyrIleArgIleHisArgIleProLysProLysArgMetLeuGlu 574

Qy 1621 TACTTCCAGGCCCACCCGGGCCGTGAACAATGGCCATCGACAAACGACACCGAGCTGCTGCAGAGC 1680
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  575 TyrPheGlnAlaThrProAlaValAlaAsnAsnGlyIleAspLysThrThrGlnLeuGlnSer 594
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Qy  1681 CTCCCTGACGAGCTGCGCGAGACAACCGCCATGCACCTGACACAAGGAGGTCCTGCGAGCTG 1740
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Db   595 LeuProAspGluLeuArgGluThrThrAlaMetHisLeuHisLysGluValLeuGluLeu    614

Qy  1741 CCACTGTTTGAGGCGGGCCCAGCCGCTGTCTGGCCCTGCGGCCC                    1800
         ||||||||||||||||||||||||||||||||||||||||||||
Db   615 ProLeuPheGluAlaAlaSerAlaArgGlyCysLeuArgLeuSerLeuAlaLeuArgPro    634

Qy  1801 GCCTTCTGCACGGCCGGGCGAGTACCTCATCCACCAAGGCAGGGCCCTGCAGGCCCCTTCTAC 1860
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Db   635 AlaPheCysThrThrProGlyGluTyrLeuIleHisGlnGlyAlaLeuGlnAlaLeuTyr    654

Qy  1861 TTTGTCTGCTCTGGCCTCCATGGAGTGGCCAACGTGGCTGCTCGCCATCCTAGGG        1920
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Db   655 PheValCysSerGlySerMetGluValAlaLeuValAlaIleLeuGly              674

Qy  1921 AAGGGCGAACCTGATGGGCTGTGCCGGCGCAGGGTGGTAAAGGGCCAATGCC           1980
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Db   675 LysGlyAspLeuIleGlyLeuCysGluLeuProArgArgGlyGlnValValLysAlaAsnAla 694

Qy  1981 GACGTGAACGGGGCGTGACGTACTGGGGTGCTCTCGCAGTGTCTGCAGTCTGGCCTGCACGAC 2040
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Db   695 AspValLysGlyGlyLeuThrTyrCysValLeuGlnCysLeuGlnLeuAlaGlyLeuHisAsp  714

Qy  2041 AGCCTTGCGCTGTACCCCGGAGTTGCCCCGCCTTCAGTGCTGTGGCCTCCGAGGGGAGCTC  2100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   715 SerLeuAlaLeuTyrProGluProAlaProAlaArgPheSerArgGlyLeuArgGlyLeuLeu 734

Qy  2101 AGCTACACACCTGGGTGCTGGGGGAGGGCTCTGCAGAGGTGGACACCCAGCTCCCTGAGCGGC 2160
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Db   735 SerTyrArgAsnLeuGlyAlaGlyGlySerAlaGluValAspThrSerSerLeuSerGly    754

Qy  2161 GACAATACCCTTATGTCACGCTCGGAGGAAGAGACAGATGGGGAGCAGGGGCCCCACG     2220
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Db   755 AspAsnThrLeuMetSerThrLeuGluGluGluGluThrAspGlyGluGlnGlyProThr    774

Qy  2221 GTCCTCCCCAGCCTGAATGAGCCCTCCAGCCCCTCGTCCCCTGGCCTGCCGACCTCC      2280
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Db   775 ValSerProLeuAlaProAlaAspGluProSerLeuProGlyCysThrSer            794

Qy  2281 TCATCCTCAGCTGCTGCCAAGCTGCTATCCCCACAGTCGAACAGCACCCCGGCCTCGTCTAGGT 2340
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   795 SerSerSerAlaAlaLysLeuLeuSerProArgSerGluProArgProArgLeuGly       814

Qy  2341 GGCAGAGGAGGGGCCCAGGGCAGGGGGGCTTTGAAGGCTGAGGCTGGCCCCCTGCTCCC    2400
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Qy  2401 CCACGGGGCCCTAGAGGGGGCTACGGCTGCCCCCCATGCCATGGAATGTGCCCCAGATCTG   2460
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Db   835 ProArgAlaLeuGluGlyLeuTyrGlyCysProProMetProTrpAsnValProProAspLeu 854

Qy  2461 AGCCCCAGGGTAGTAGATGGGCAATTGAACGGCGTGTGCTTCCGGACCCACCCCAAGTTCTCT 2520
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Qy  2521 TTCCGGGCTGGGGCCCAGTCTGGCCCCGGAATGTAGCCAGCCAGCCCTCCCCTGGACCAGAGACC 2580
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Db   875 PheArgValGlyGlnSerGlyProGluCysSerSerSerProGlyProGlySer          894

Qy  2581 GGCCTGCTCACTGTTCCCCATGGGCCAGCCGAGGCAAGAGACAACACACTGGACAAG       2640
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   895 GlyLeuLeuThrValProHisGlyProSerGluGlnLeuAlaArgAsnThrAspThrLeuAspLys 914

Qy  2641 CTTCCGCAGGGGTGACGAGCTGTCAGAGGACTGCAG                            2700
         ||||||||||||||||||||||||||||||||||||
Db   915 LeuArgGlnAlaValThrGluLeuSerGluGlnValLeuGlnMetArgGluGlyLeuGln    934

Qy  2701 TCACTTCGCCAGGCTGTGCAGCTTGTCCTGCGGGCCCACAGGGGAGGGGTCCGTGCCCCTCGG 2760
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   935 SerLeuArgGlnAlaValGlnLeuValAlaProHisArgGluGlyProCysProCysProArg  954

Qy  2761 GCATGGGAGGAGAGGGGCCGTGCCCAGCCACACTCCCGGGCTTCTGCAGCCTCTGTGTGGTG  2820
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Db   955 AlaSerGlyGluGlyLeuProCysGlyProAlaSerThrSerGlyLeuLeuGlnProLeuGlyLeuValLeuGlnLeu 974

Qy  2821 GACACTGGGGCATCCTCCTACTCCCTGCCTGCAGAGCCCCCAGCGTGGCCTCGTCCTTGTCTTGAGTGGGACT 2880
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   975 AspThrGlyAlaSerSerTyrCysLeuProAlaGlnSerProAlaGlySerValLeuSerGlyThr        994

Qy  2881 TGGCCCACCCTCGGTCCGGGGGCCCCTCCCCCCATGGCACCCTGCCCTGCGGGGTCCCCA    2940
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   995 TrpProHisProArgProGlyProProProLeuMetAlaProThrProProTrpGlyProPro   1014

Qy  2941 GCCGTCTCAGAGCGTCCCCCTGGCCTCCGAGACCCACAGCTTTCTGGACTTCCACCCTCAGACTCA 3000
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1015 AlaSerGluSerSerProTrpProAlaThrAlaLeuPheTrpThrSerThrSerAspSer      1034

Qy  3001 GAGCCCCCTGCCTCAGAGAGACCTTCTGCTTGAGCCGCCAGCACCCCTGCCTCCCTCCTCCTCT  3060
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1035 GluProProAlaSerGlyAspLeuCysSerGluGlyProSerThrProAlaSerProPro     1054

Qy  3061 TCTGAGGAAGGGGCTAGGACTGGGCCCCGCGCAGAGGCCTGTGCAGAGGCTGAGGGCTACCAGC  3120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1055 SerGluGluGlyAlaArgThrGlyProArgAlaGluProValSerArgGlnAlaAlaThrSer   1074

Qy  3121 ACTGGAGAAGCCCCCACCAGGGGTCAGGGGGCGGGGCCTGGCCCCGGGGCTGCTGCCCACAGCCTG 3180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1075 ThrGlyGluProProGlySerGlyValGlyLeuAlaLeuAlaLeuProProProHisSerSerLeu 1094

Qy  3181 GAGATGGTGCTTATTGGGTGCCATGGGTCTTCTGGCCACAGTCCCAGTGGGACCCAGAAGAAGGC  3240
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1095 GluMetValLeuIleGlyCysHisGlySerSerGlyThrValGlnNrpThrGlnGluGluGly    1114

Qy  3241 ACAGGGGTC 3249
         |||||||||
Db  1115 ThrGlyVal 1117
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RESULT 2
O89047
ID   O89047   PRELIMINARY;   PRT;   1087 AA.
AC   O89047;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ELK channel 2 (Potassium channel).
GN   ELK2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=CORTEX;
RA   Engeland B.; Neu A.; Ludwig J.; Roeper J.; Pongs O.;
RT   "Identification of three rat potassium channel genes homologous to D.
RT   melanogaster elk.";
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 120-273 FROM N.A.
RX   MEDLINE=98382545; PubMed=9714851;
RA   Shi W.; Wang H.S.; Pan Z.; Wymore R.S.; Cohen I.S.; McKinnon D.;
RA   Dixon J.E.;
RT   "Cloning of a mammalian elk potassium channel gene and EAG mRNA
RT   distribution in rat sympathetic ganglia.";
RL   J. Physiol. (Lond) 511:675-682(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99386988; PubMed=10455180;
RA   Miyake A.; Mochizuki S.; Yokoi H.; Kohda M.; Furuichi K.;
RT   "New ether-a-go-go K+ channel family members localized in human
RT   telencephalon.";
RL   J. Biol. Chem. 274:25018-25025(1999).
DR   EMBL; AJ007627; CAA07586.1; -.
DR   EMBL; AF073892; AAC61522.1; -.

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DR   EMBL; AB022697; BAA83591.1; -.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM000086; PAC; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50042; cNMP_BINDING_3; 1.
KW   Ionic channel.
SQ   SEQUENCE   1087 AA;  117579 MW;  16B5AFFC3B0A405B CRC64;
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Alignment Scores:
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                      Pred. No.:              1.11e-293
                      Score:                  5428.00
                      Percent Similarity:     96.60%
                      Best Local Similarity:  95.58%
                      Query Match:            89.14%
                      DB:                     11
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                                Length:        1087
                                Matches:       1039
                                Conservative:  11
                                Mismatches:    33
                                Indels:        4
                                Gaps:          2
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US-09-965-830-1_COPY_6_3257 (1-3252) x 089047 (1-1087)

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Qy      1 ATGCCGGCCATGCAGGGGGCCTCCTGGGCCCTCAGACACCTTTCCTGGACACCATCGCTACG 60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetProAlaMetArgGlyLeuLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy     61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAAGCCCAGTGGGCGGGGGCTCTTC 120
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyLysAlaGlyArgGlyLeuPhe 40

Qy    121 CCCGTGGTCTACTGCTCTACGGGCTTCTGTGACCTCACGGGCCGTTCCTCCGGGGCTGAGGTC 180
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     41 ProValValTyrCysSerArgGlyPheCysAspLeuThrGlyPheSerArgAlaGluVal 60

Qy    181 ATGCAGCCGGGGGGCTGTGCCCTGCGTCCCTTCCTTTATGGGGCCCAGACCTCGTCCGC 240
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MetGlnArgGlyCysAlaCysSerPheLeuTyrGlyProAspThrSerGluValValArg 80

Qy    241 CAACAGATCCGCAAGGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGATCCTGTAC 300
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 GlnGlnIleArgLysGlyAlaLeuAspGluHisLysGluPheLysAlaGluLeuIleLeuTyr 100

Qy    301 CGGAAGAGCGGGGGCCTTCCCGTTCTGGGTGTCTCCGGATGTGATACCCATAAAAGAATGAGAA 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 ArgLysSerGlyGlyLeuProPheTrpCysLeuLeuAspValIleLeuProIleLysAsnGluLys 120

Qy    361 GGGGAGGTGGCGTCTCTTCCTACTCTCTCACAAGGACCATCAGGAGCCGGAACCGGAG 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GlyGluValAlaLeuLeuPheLeuuValSerHisLysAspIleSerGluThrLysAsnArgGly 140

Qy    421 GGCCCCGACAGGAGGAGACAGGTCGTTGCCGGCGCCCGAGATATGCCGGGGGCACGATCC 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 GlyProAspAsnTrpLysGlnArgGlyGlyGlyValArgArgArgTyrArgGlyAlaGlySer 160

Qy    481 AAAGGCTTCAATCCAACCGGCGCGGGAGCCGGTGCCTACCACCGTGTCCGCAGC 540
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    161 LysGlyPheAsnAlaAsnArgArgGlyArgGlnAlaValLeuuTyrHisLeuSerGlyHis 180

Qy    541 CTGCAGAAGCAGCCCAAGGGGACAAGACTCAATAAGGGTGTTTGGGGAGAAACCA 600
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 LeuGlnLysGlnProLysGlyLysLysHisLysGlyValPheGlyGluLysPro 200

Qy    601 AACTTGCCTGAGTACAAAAAGTAGCCGCCGGAAGTCGCCTTCATCCTGTTGCACTGT 660
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    201 AsnLeuProGlnTyrLysValAlaAlaGlySerProPheIleLeuLeuHisCys 220

Qy    661 GGGGCACTGAGAGCCACCTGGGANGGGCTTCATCCTGCTCGCCACACTCTATGTGGCTGTC 720
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Db    221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuLeuAlaThrLeuTyrValAlaVal 240
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Qy    721 ACTGTGCCCTACAGCGGCGTGTGTGGAGCACAGACAGGGGAGCCCAGTGCCCGCCCGGGCCG 780

Db    241 ThrValProTyrSerValCysValSerThrAlaArgGluProSerAlaAlaArgGlyPro 260
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Qy    781 CCCAGCGTCTGTGACCTGGCCCGGGAGGTCCTCTTCATCCTGGACATTGTGCTGAATTTC 840

Db    261 ProSerValCysAspLeuAlaArgGluValLeuPheIleLeuAspIleValLeuAsnPhe 280
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Qy    841 CGTACCCACATTCGTTCGCCAAGTCCGGGGTGTTGGTTTGCCCGCAAAGTCCATTTGCCTC 900

Db    281 ArgThrThrPheArgPheValSerLysGlyGlnValValGlyLeuPheIleLeuLeuAsnPhe 300
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Qy    901 CACTACGTCACCACCTGGTTCCTTGCTGGATGTCATCGGAGGCTGCGCTTTGACCTGCTA 960

Db    301 HisTyrValThrThrTrpPheLeuAlaGlyCysHisLeuLeuLeuLeuProPheAspLeuLeu 320
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    961 CATGCCTTCAAGGTCAAGGTGTACTTCGGGGGCCCATCTTCTGCTGAAGAACGGTGCCCTTCTG 1020

Db    321 HisAlaPheLysValLysValTyrPheGlyGlyProSerSerAlaGluGluArgValAlaLeu 340
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Qy   1021 CGCCTGCTGCGCGCCCTGCTTCCGGCGCTGACACGGTTACTCGGACTACAGGCCCGTGGCTGC 1080

Db    341 ArgLeuLeuArgLeuLeuProArgLeuAspArgTyrSerGlnTyrSerAlaValValLeu 360
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1081 ACACTGCTCATGGCCGTGTTCGCCGCCCTGGGCCCAGCCCCACTGGTGTCCTGGTTTTTAC 1140

Db    361 ThrLeuLeuMetAlaValPheAlaAlaLeuGlyProAlaProLeuValSerTrpTyr 380
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Qy   1141 ATTGCCCACGCGGGAGAATCGAGAGGCAGGAGCGGAATCCGAGCTGCCTGAGAATTGGCCTGCAG 1200

Db    381 IleGlyGlnGlnIleGluGlnAsnSerGluSerGlnLeuProGluIleGlyTyrLeuGln 400
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1201 GAGCTGGCCGCCGCCGACGACTGGAGACTCCCCACTACCTGTGGGCCGGAGGCCCAGCGTGGAGGG 1260

Db    401 GluLeuAlaArgArgLeuProGluThrProTyrTyrLeuValSerArgSerProAspGlyGly 420
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1261 AACAGCTCCGGCAGAGTGACAACTGCAGCAGCAGC---------AGGGAGGCCAACGGG 1311

Db    421 AsnSerSerGlyGluSerCysSerSerSerGlyGlyGlyLysGluAlaAsnGly 440
          ||||||||||||||||:::|||||||||||||||||        |||||||||||||||||
Qy   1312 ACGGGGGCTGGAGCTGCTGGGGCGGGGGGGGTGCTGCCGCAGCCGCTACATCACCTCCTCTAC 1371

Db    441 ThrGlyLeuGluLeuLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr 460
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1372 TTCGGCCACTCAGCAGCCTCACCAGCAGCGTGGCCTTCGGCAACGGTCCGCCAACACGGACACC 1431

Db    461 PheAlaLeuSerSerLeuThrSerSerValGlyPheGlyAsnValSerAlaAsnThrAspThr 480
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy   1432 GAGAGAGATCTTCTCCATCTGCACACAATGCTCATCGGCCGCCTGATCGCCGAGTGGTGTTT 1491

Db    481 GluLysIlePheSerIleCysThrAspMetLeuIleGlyArgLeuIleAlaGluValProPhe 500
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Qy   1492 GGGAACGTGACGGCCATCATCCAGGCGCATGTACCCCGCGCTTTGTTCTGTGTACCACAGCCGC 1551

Db    501 GlyAsnValThrAlaIleIleGlnAlaHisValProArgPheLeuuTyrHisSerArg 520
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Qy   1552 ACGCGCGACCTGCGCCGACTACATCCGCATCCAAGCCGCTATCCCAAGCAGCGC 1611

Db    521 ThrArgAspLeuArgArgTyrIleArgIleGlnAlaAlaIleProLysGlnArg 540
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Qy   1612 ATGCTGGAGTACTTCCAGGCCACCTGGGCGGCCACTGGCATGCAACCTGACACACCGAGCTG 1671

Db    541 MetLeuGluTyrPheGlnAlaThrTrpAlaAlaThrGlyMetGlnProAspThrThrGluLeu 560
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Qy   1672 CTGCAGAGCCTCCCGTGACGAGCCGCGACGACATGCCAGACTGCACAAGGAGGTC 1731

Db    561 LeuGlnSerLeuProAspGluLeuuArgAlaAspIleAlaMetHisIleLeuHisLysGluVal 580
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Qy   1732 CTGCAGCTGCCACTGTTTGAGGCGCGCCAGCCGCCACTGTCTCTGGCC 1791
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Db   581  LeuGlnLeuProLeuPheGluValAlaAlaSerArgValCysLeuArgLeuSerLeuuAla  600

Qy  1792  CTGCGGCCGCCGCTTCTCCACGCCGCGGGCGAGTACCTCATCCACCAAGGCGATGCCCTGCAG  1851
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   601  LeuArgProAlaPheCysThrProGlyGluTyrLeuIleHisGlnGlyAspAlaLeuGln  620

Qy  1852  GCCCCTCTACTTTGTCTGCTTGGCCTCCTCCGGAGAGGTGCTCAAGGTGGCCACCGTGCTGCC  1911
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   621  AlaLeuTyrPheValCysSerSerGlySerMetGluValLeuLysGlyGlyThrValLeuAla  640

Qy  1912  ATCCTAGGGAGGGGACCTGATCGGCGTCTGTGAGCTCCCCGGGGAGCAGGTGGGTAAAG  1971
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Db   641  IleLeuGlyLysGlyAspLeuIleGlyCysCysGluLeuProGlnGluArgGluLeuValGly  660

Qy  1972  GCCAATGCCGACGTGAAGGGGCTGACGTACTGCGTCCTGCAGTGTGCCCTGGGCTGGC  2031
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Db   661  AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysAlaLeuGlyTrpGly  680

Qy  2032  CTGCACGACAGCCTTGGCGTCGTACCCCGAGTTGCCCGCCGCTTCAGTCGTGGCCTTCCGA  2091
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Db   681  LeuHisGluSerLeuAlaLeuValThrTyrProGluPheAlaAlaProArgPheSerArg  700

Qy  2092  GGGGAGCTCAGCTACAACCTGGGTGCTGGGGGAGGCTCTCGAGAGTGTGGACACCAGCTCC  2151
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Db   701  GlyGluLeuSerTyrAsnLeuGlyAlaGlyValSerAlaGluValAspThrSerSer  720

Qy  2152  CTGAGCGCGGCCACAATACCCTTAGTCGTCCACGCCTGGGAGGAGGAGGACAGAGATGGGAGCAG  2211
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Db   721  LeuSerGlyAspAsnThrLeuMetSerThrLeuValGluLysGluThrAspGlyGluGln  740

Qy  2212  GGGCCCAGGCTGTCCCCCAGCCCACTGATGAGCCCTCCAGCCCCCTGCTAGTCGTCCCCTGGC  2271
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Qy  2272  TGCACCTCCTTCATCCTCAGCTGCCAAGCTGCTATCCCACGTTGGAACACGACACCCCGGCCT  2331
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   761  CysThrSerSerSerSerLeuAlaAlaLysLeuLeuSerProArgArgThrAlaProArgPro  780

Qy  2332  CGTCCTTAGGTGGCAGAGAGGGGCAGGCAGGGGCTTTGAAGGCTGAGGCTGGCCCCC  2391
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Db   781  ArgLeuGlyGlyArgGlyArgProSerArgGlyAlaGlyValLeuLysGlyGluAlaGlyPro  800

Qy  2392  TCTCGTCCCCCAGGGGCCCTAGAGGGGCCTACGGCCCCATGCCCATGGGAAGTGCCC  2451
          |||||::::||||||||||||||||||||||||||||||||||||||||
Db   801  SerAlaLaHisProArgThrLeuAspGlyLeuGlnLeuProProMetProTrpPAsnValPro  820

Qy  2452  CCAGATCTGAGCCCCAGGGTAGTGAGACGGCTGTGGCTGTGGACCAGCCC  2511
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Db   821  ProAspLeuSerProArgValValAspSerGlyLyrIleGluAspGlyCysGlySerAspGlnHis  840

Qy  2512  AAGTTCTCTTTCCGCGTGGGGCCCAGTCTGGCCGAATGTAGCAGCAGCCCCCTCCCCCTGGA  2571
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Db   841  LysPheSerPheArgValGlyGlnSerGlyProGluCysSerSerSerProSerProGly  860

Qy  2572  CCAGAGACGGGCGGCCTGAGCTCACTGTTCCCCATGGGCCCCAGGGCCAAGGAACACAGACACA  2631
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   861  ThrGluSerGlyLeuLeuThrValProLeuuValProSerGlyAlaLeuArgAsnThrAspThr  880

Qy  2632  CTGGACAAGCTTCGGCCACGGCGGTCACAGAGCGGTTGCTCAGAGCGATGCGGGAA  2691
          ||||||||||||||||||||||||||||||||||||||||||||||||
Db   881  LeuAspLysLeuArgProArgArgSerGlnSerGlyCysSerGluArgMetArgGlu  900

Qy  2692  GGACTGCAGTCACTTCCGCCAGCTGTGCGCCGTGTTCCTGGCGCGCCCACAGGGAGGGTCCG  2751
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   901  GlyLeuGlnSerLeuArgGlnAlaValAlaGlnLeuLeuuLeuValProGlyGlyGlyGln  920

Qy  2752  TGCCCCTCGGGACATCGAGCCAGCCACTTCCCGGGCTTCTGCCGGCTTTGCAGCCT  2811
          ||||||||||||||||||||||||||||||||||||||||||||||::::
Db   921  CysProArgValSerGlyValGlyLyrProCysProGlnAlaThrAlaSerGlyLeuLeuGlnPro  940

Qy  2812  CTGTGTGTGGACACTGGGGACCGGGCATCTCCTTCCTTACTGCCTCGCAGCCCCAGTGGCTGTCTTG  2871
          ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db   941  LeuArgValAspThrGlyAlaSerSerTyrCysLeuGlnProProAlaGlySerValLeu  960
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RESULT 3

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Qy  2872  AGTGGGACTTGGGCCCCCACCCTCGTCCCGGGG----CCTGCTCCCCTCCATGGCACCCTGGCCC  2928
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Db   961  SerGlyThrTrpProHisProArgProGlyHisProProProLeuMetAlaProThrPro  980

Qy  2929  TGGGGTCCCCCAGGGGTCTCAGAGTCTCCCCGTCCCTGGCGGTGGCCACAGCTTTCTGACCTCC  2988
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Db   981  TrpGlyProProAlaSerGlnSerSerProThrProTrpProAlaProArgAlaThrAlaLeuThrProSer  1000

Qy  2989  ACCTCAGACTCAGAGACCCCCTGCCTCTCAGGAGACCTTCGCTCTGAGCCCAGCACCCCCTGCC  3048
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Db  1021  SerProProProGluGluGlyLeuGlyLeuAlaProValSerGlnAla  1040

Qy  3109  GAGGCTACCAGCACTGGGAGAGCCCCCACCAGGGTTCAGGGGCCTTGCCCTGGGAC  3168
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Db  1041  GluAlaThrSerThrGlyGluProProThrGlyLyrThrProAlaProValSerGlnAla  1060

Qy  3169  CCCCACAGCCTGGAGAGGTTGCTTATTGGCGTCCTGCCCCATGGGTCTGCGGGCAGTCCACTGGAC  3228
          |||||||||||||||||||||||| || ||||||||||||||||||||||||
Db  1061  ProHisSerLeuGluMetValLeuLeuIleGlyCysHisGlyTyrProGlySerValGlnTrpThr  1080

Qy  3229  CAGGAAGAAGGCACAGGGGTC  3249
          |||||||||||||||||||||
Db  1081  GlnGluGluGlyThrGlyVal  1087
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Alignment Scores:

Pred. No.:	
Score:	5.14e-293
Score:	5416.00
Percent Similarity:	96.41%
Best Local Similarity:	95.40%

Length:	1087
Matches:	1037
Conservative:	11
Mismatches:	35

Query Match: 88.958%   Indels: 4
DB: 11   Gaps: 2

US-09-965-830-1_copy_6_3257 (1-3252) x Q9WJ0 (1-1087)

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Db      1 MetProAlaMetProGlyLeuLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy     61 CGCTTCGACGGCACGCACAGTAACTTCGTGCTGGGCAACCCCAGGTGGGGGGGGGTCTTC 120
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Db     21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlyLeuPhe 40

Qy    121 CCCGTGGGTCTACTGCTCTCTGATGGCTTCTCCGGGCTCAGGTC 180
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Db     41 ProValValTyrCysSerAspGlyPheCysGlyPheSerArgAlaGluVal 60

Qy    181 ATGCAGCGGGGCGGTGCCCTGCCTGGCCAGAGACCAGTGAGCTCGTCCGC 240
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Db     61 MetGlnArgGlyGlyCysAlaCysSerPheLeuThrGlyLeuProAspThrSerGluLeuValArg 80

Qy    241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGACCTGATCCTGTAC 300
          ||||||||||
Db     81 GlnGlnIleArgLysAlaLeuAspGluHisLysGluPheLysAlaAspLeuIleLeuTyr 100

Qy    301 CGGAAGAGCGGGGCCTCCGGTTCTGGTGTCTCCTGGATGATACCCATAAAGAATGAGAAA 360
          ||||||||||
Db    101 ArgLysSerGlyLeuProPheTrpCysLeuLeuAspHisValIleProIleLysAsnGluLys 120

Qy    361 GGGGGAGGTGGCTCTCTTCCTTAGTGCTCACAAGGACAACATCACCGAAACCAAGAACCCAGGG 420
          ||||||||||
Db    121 GlyGlyValAlaLeuLeuPheLeuValSerHisLysAspAsnIleSerGluThrLysAsnArgGly 140

Qy    421 GGCCCCGACAGCATGGAAGGAGACAAGGTTGGTGGCGGCCCGATATGCCGGGCACGATCC 480
          ||||||||||
Db    141 GlyProAspSasnTrpLysGluArgGlyLyGlyAlaGrgArgTyrGlyArgAlaGlySer 160

Qy    481 AAAGGCTTCAATGCCAACCGGCGGCGGAGCCGGGCCGTGCGTCTACACCTGTCCGGGCAC 540
          ||||||||||
Db    161 LysGlyPheAsnAlaAsnArgArgArgSerArgAlaValLeuTyrHisLeuSerGlyHis 180

Qy    541 CTGCAGAAGCAGCCCAAGGGAAGCAAGCACAAGAGTTCAAATAAGGGGGTGTTTGGGGAGAAACCA 600
          ||||||||||
Db    181 LeuGlnLysGlnProLysGlyValTyrLysHisLysLeuLeuAsnLysGlyValPheGlyGluLysPro 200

Qy    601 AACTTGCCTGAGTACAAAGTAGGCGCCATCCGGGAAGTCGCCCTTCATCCTGTTGCACTGT 660
          ||||||||||
Db    201 AsnLeuProGluTyrLysValGlyAlaIleAlaGluSerProPheIleLeuLeuHisCys 220

Qy    661 GGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCCCACACTCTATGTGGGCTGTC 720
          ||||||||||
Db    221 GlyAlaLeuArgAlaThrTrpAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 240

Qy    721 ACTGTGCCCTACAGCGGTGTGTGGTGTGGAGCAGCACGGGACCCCAGTGCGCGCCCCGCCCG 780
          ||||||||||
Db    241 ThrValProTyrSerValCysValSerThrAlaAlaArgGluHisGlyAspAlaLeuGln 260

Qy    781 CCCAGGCGTCTGTGACCTGGCCTGGGAGGTCCCTCTTCANCCTTGACAANTTGTGTGAATTTC 840
          ||||||||||
Db    261 ProSerValCysAspLeuAlaValGluValLeuPheLeuIleLeuAspAsnPhe 280

Qy    841 CGTACCACCATTCGTGTCTCCAAGTCGGGGCCCAGGTGGGTTGTTTGCCCAAAGTCCANTTTGCCTC 900
          ||||||||||
Db    281 ArgThrThrPheLeuValSerLysSerGlyValPheAlaLysSerIleCysLeu 300

Qy    901 CACTACGGTCACCACCTGGTTCCGTGGATTGGATGTCATCGACGGCGTCGCCCTTTGACCTGCTA 960
          ||||||||||
Db    301 HisTyrValThrThrTrpPheLeuGluAsnValIleIleAlaIleAlaLeuProPheAspLeuLeu 320

Qy    961 CATGCCTTCAAGGTCAACGTGTACTTCGGGGGCCCCATCTCTGCTGAAGACGGTGCGCCTGCTG 1020
          ||||||||||
Db    321 HisAlaPheLysValAsnValTyrValGlyAlaHisIleLeuLeuLysThrValArgLeuLeu 340
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Qy   1021 CGCCTGCTGCTGCCTGCTTCGCGGGCGTACTCGCGGGTACTCGCAGTACACGCGGTGCTG 1080
          ||||||||||
Db    341 ArgLeuLeuGlyLeuLeuProArgArgLeuAspAspArgTyrSerArgValTyr 360

Qy   1081 ACACTGCTTCATGGCCTGGTGTGCCCGTGGTTCCGCCTGCTCGGGCCCGACTGGGGTCGGCCGTGGGGTTTTAC 1140
          ||||||||||
Db    361 ThrLeuLeuMetAlaValPheAlaLeuLeuAlaHisTrpLeuAlaCysValTrpPheTyr 380

Qy   1141 ATTGGCCAGCAGGGAGGAGTCGAGAGGCAGCAGAAATCCGAGCTGCCCTCCAGAATTGGGCTGCTCCAG 1200
          ||||||:||||
Db    381 IleGlyGlnGlnGlyGluValGluArgGlnGlnLysSerGluLeuProLeuArgTrpLeuGln 400

Qy   1201 GAGCTGGGCCCGCCGGACTGGAGACTCCCTACTACCTGGTTGGGGGGCCGGGGAGGCGGAGG 1260
          ||||||||||
Db    401 GluLeuGlyAlaAlaAspTrpArgLeuProTyrLeuValSerArgSerProAspGlyGly 420

Qy   1261 AACAGCTCCGGCCAGAGTGACAGCTGCAACTGCAGCAGCAGC----------AGGGAGGGCCAACGG 1311
          ||||||||||                                         |||
Db    421 AsnSerSerGlyGlnSerAspSerSerSerSerGlyGlyGlyValGlySerGluLeuAlaAsnGly 440

Qy   1312 ACGGGGCTGGAGGTGCTGGGGGGCCGGGCGTGCGTGCGGCCAGGCCGCTACAATCACCTCCCTCTAC 1371
          ||||||||||
Db    441 ThrGlyLeuGluValLeuGlyGlyProSerLeuArgSerAlaTyrIleThrSerLeuTyr 460

Qy   1372 TTCGCACTCAGCAGCCCTCACCAGCGTGGCGGCTTCGGCAAGTGTCCGCCAACACGGACACC 1431
          ||||||||||
Db    461 PheAlaLeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspThr 480

Qy   1432 GAGAAGATCTTCTCCATCTGCACCATGCTCATTGGGCCCCTGATGCACGGGGTGGTGTTT 1491
          ||||||||||
Db    481 GluLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMetHisAlaValPhe 500

Qy   1492 ACGGGGAACGTGACGGCCCATCACCATGATACCAGGTACATGTACCGCCGCTTCTGTACCAGAGCCGC 1551
          ||||||||||
Db    501 ThrGlyAsnValThrAlaHisHisHisMetTyrValAlaArgPheLeuTyrHisSerArg 520

Qy   1552 ACGGGCGACCTGCCGACTACACATCCGCCATCCACCGTATCCCAAGCCCCTCCAGCGC 1611
          ||||||||||
Db    521 MetGlyAspLeuProThrThrHisProAlaValAsnAsnGlyIleLeuAspThrThrGluLeu 540

Qy   1612 ATGCTGGAGTACTTCCAGGCCACCATCATGGAGCTCCGCGAGCAGCTCCGGCGAGACGGC 1671
          ||||||||||
Db    541 MetLeuGluTyrPheGlnAlaThrIleMetGluLeuArgGluGlnLeuArgArgThrGlu 560

Qy   1672 CTGCGGAGGCCTCCCTGACCAGCGCTCGCGGCAGCATCACCACGTGACACAAGAGAGGTC 1731
          ||||||||||
Db    561 LeuArgArgProLeuProGlyLeuGluTyrLeuIleHisGlnGlyAspAlaLeuGln 580

Qy   1732 CTGCAGGCTGCCACTGCTTTTGAGGGCGGCGGCCAGCCGCCCAGCGCGCACTGTCTCTGGCC 1791
          ||||||||||
Db    581 LeuGlnLeuProLeuProGluGluAlaAlaSerArgGlyCysGlyLeuGlnLeuAlaAla 600

Qy   1792 CTGCCGGCCCGGCTTCTGCACGCGGGCGAGTACCTTCATCCACCAAGGCGGGATGCCCTGCAG 1851
          ||||||||||
Db    601 GlyAlaLeuArgAlaThrArgAspGlyPheIleLeuLeuAlaThrLeuTyrValAlaVal 620

Qy   1852 GCCCTTCTACTTTGTCTGCTCTGGCTGTCCCCATGGAGGTGGTGGGCACCGTTCGTGCGC 1911
          ||||||||||
Db    621 AlaLeuLeuTyrPheValCysSerSerGlySerMetGluValValLeuGlyTyrThrValLeuAla 640

Qy   1912 ATCCTAGGGAGAAGGGCGGACTGAATCGGCTGGTGTGAGCGTGGCCCCGGGGAGAGCTGGACTGAAAG 1971
          ||||||||||
Db    641 IleLeuGlyGlyLysGlyAspTrpLeuGlyCysGlyLeuProGlnAsnArgGlnGlnValValLys 660

Qy   1972 GCCAATGCCGACGTGAAGGGCTGACGTACTGCGTCCTGCAGTGTCTGCACTGGCTGGC 2031
          ||||||||||
Db    661 AlaAsnAlaAspValLysGlyLeuThrTyrCysValLeuGlnCysLeuHisTrpLeuAlaGly 680

Qy   2032 CTGCAGCACAGCCTTGCGCTGCTGTACCCCGAGTTTGCCCGCGCCTTCAGTCGGTGGGCTCCGA 2091
          ||||:::||
Db    681 LeuHisGluSerLeuAlaLeuLeuTyrProGluPheAlaProArgPheSerArgGlyLeuArg 700

Qy   2092 GGGGAGCTCAGCTACAACCTGGCTGCTGGGGGGAGGGCTCTGCAGAGGTGGGACACCAGCTC 2151
Db   2092 GlyGlySerLeu                                              2151
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RESULT 4

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ID   Q96L42
AC   Q96L42;
DT   01-DEC-2001 (TREMBLrel. 19, Created)
DT   01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT   01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE   Ether-a-go-go-like potassium channel 1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RA   Baxter D.F., Kirk M., Garcia A.F., Raimondi A., Holmqvist M.H.,
RA   Bojanic D., Distefano P.S., Curtis R., Xie Y.;
RT   "A novel membrane potential-sensitive fluorescent dye improves cell-
RT   based assays for ion channels.";
RL   Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY053503; AAL15429.1; -.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000014; PAS_domain.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF07885; PAC; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS00229; CNMP_BINDING_3; 1.
KW   Ionic channel.
SQ   SEQUENCE   1107 AA;   123832 MW;   4DC93EF85B674905 CRC64;
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Q96L42                           PRELIMINARY;      PRT;   1107 AA.
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Alignment Scores:
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Pred. No.:
Score:                  1.31e-132
                        2529.50         Length:            1107
Percent Similarity:     60.24%          Matches:           559
Best Local Similarity:  47.49%          Conservative:      150
Query Match:            41.54%          Mismatches:        267
                                        Indels:            201
                                        Gaps:              27
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US-09-965-830-1_copy_6_3257 (1-3252) x Q96L42 (1-11107)

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Qy    1 ATGCCGGCCATGCGGGCGCCTCTGGCCGCCCTCAGAAACACCTTCCTGGACCATCGCTACG 60
          |||||       ||:::|||||||||||||||||||||||||||||||||||||||| |||
Db    1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy   61 CGCTTCGACGGCGCACGCAGTAACTTCGTTGGTGGGCGAACGCCCAGGTGGGCGGGGCTTTC 120
          ||||||||| ||  |||||||||||||||||||||||:||||| |||  ||||||  || |
Db   21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnValAlaLysGlyPhe 40

Qy  121 CCCGTGGTCTACTGCTCTGATGGCTTCTGTGACCTCACGGGGCTTCTCCCGGGCCTGAGGTC 180
          ||||||||||||||||||||||||||||:|||||||||||||||||  |||  ||||||||
Db   41 ProIleValTyrCysSerAspGlyPheCysAspLeuThrGlyLeuLeuProGlyLeuArgVal 60

Qy  181 ATGCACGCGGGCGTGGCCTGCCTCTCCTTTATGGGCGAGCAGAACACCAGTGAGCTGCCGG 240
          ||| |::|||||  |||||||||||:|||||:||||||||||||||||||||||||||||||
Db   61 MetGlnLysGlyCysSerCysLysSerPheLeuPheGlyValAlaThrGlnAlaArgThrGlu 80

Qy  241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGCTGAGCTGCTAC 300
          |||||:  |||::||:||||||||||||:|||||||||||||:||||::||:|:|||||||
Db   81 LeuGlnIleGluLysSerLeuGluGluHisLysGluPheLysGlyGluLeuSerSerTyr 100
```

```
Qy    301  CGGAAGAGCGGGCCTCCGGTTCTGGTGTCCTGATGTGATACCCATAAAGAATGAGAAA  360
           :::||||||||| ||||
Db    101  LysLysAsnGlySerProPheTrpCysLeuLeuAspIleValProIleLysLysAsnGluLys  120

Qy    361  GGGGAGGTGGCTCTCTCCAGTGTCTCTCACAGGACAATCACAGAAACCGAGGG  420
           ||||||||||||||||||||||||||||||||||||||||||  :::
Db    121  GlyAspValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle  140

Qy    421  GGCCCCAGAGATGGAGAGGAGAGGAGAGAGGTGGGCCGGGACGATCC  480
           |||||||||||||||
Db    141  ThrProGluAspLysLysGluAsp---------------LysValLysGlyArgSerArgAla  156

Qy    481  ---AAAGGCTTCAATGGCACCGGGCCGGGACCGTGCTCTACCACCTGTCCGGG  537
           ::: |||
Db    157  GlyThrHisPheAspSerAlaArgArgSerArgAlaAlaValLeuTyrHisIleSerGly  176

Qy    538  CACCTGCAGAAGCAGCCCAAGGGGCCAAGCACAACAAGCTCAATAAGGGGGTGTTTGGGAGAA  597
           |||||||||||||||||||||
Db    177  HisLeuGlnArgGlnLysLysAsnLysLysLeuLysIleAsnAsnAsnValPheValAspLys  196

Qy    598  CCAAAACTTGCCTCAGTACAAAAGTAGCCGCCCATCGGAAGTGCCCTTCATCCTGTTGCAC  657
           :::||||   |||||
Db    197  ProAlaPheProGlnTyrLysSerArgAspAlaLysLysSerLysSerPheIleLeuLeuHis  216

Qy    658  TGTGGGGACACTGAGAGCCCACCTGGGATGGCTTTCATCCTGTTCGACCACTCTATGTGGCT  717
           :::||||||||||||
Db    217  PheSerThrPheLysAlaGlyThrAspProThrLysLeuLeuLeuLeuAlaThrPheTyrValAla  236

Qy    718  GTCACTGTGCCCTACAGCGTGTGTGTGAGCACACAGCCACGTGCCCCCGGC  777
           ||||||||||
Db    237  ValThrValProTyrAsnValCysSerPheIleGlyAsnAspAspLeuSerThrThrArgSer  256

Qy    778  ---CCGCCCAGGCTCTGTCGAACCTGGACCTGGCCCTGGAGGTCCCTCTTCATCCCTGGAAT  837
           :::||||||||
Db    257  ---ThrThrValSerAspIleAlaValGlyIleLeuPheIleLeuAspValIleLeuLeuAsn  275

Qy    838  CTACATGCCTTCAAGGTCACACGGTACTTCGGGGCCCATCTGCTGAAGACGGTGCCGCCTG  897
           ::: ||||||||
Db    276  PheArgThrThrTyrAsnValCysSerGlyValHisLeuLeuLeuPheGluAlaArgSerLeu  295

Qy    898  CTCCACTACGGTCACCACCTGGTTCCTCCTGGATGTCATCGCAGCGGCTGCCCTTTGACCTG  957
           :::||||||||||||
Db    296  IleHisTyrValThrThrTrpPheIleIleLeuAspLeuIleAlaAlaAlaLeuProPheAsnLeu  315

Qy    958  CTACAGCCCTTCAAGGTCAACGTGACTCTCGGGGCCCCATCTGCTGAAGACGGTGCCGCCTG  1017
           |||||||||||
Db    316  LeuTyrAlaPheAsnValThrValValSerLeuValHisLeuLeuTyrValArgLeu  335

Qy    1018 CTGCGCCTGCTGCGCCTTGCCTTCCGCGCGGTACTCAGCGCCGTGGTG  1077
           ||||||||||||
Db    336  LeuArgLeuLeuArgLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrIleVal  355

Qy    1078 CTGACACTGCTCATGGGCCGTGTTCGCCCGACTGGCTGCCGTCTGGTTT  1137
           ||||||||||||
Db    356  LeuThrLeuLeuMetSerMetPheAlaLeuLeuAlaHisTrpMetAlaCysIleThrProTyr  375

Qy    1138 TACATTGGCCCACGGGAGACATCGAGAGCAGCAGAATCCGAGCTGCCTGAGATTGGCTGGCTG  1197
           |||||||||||
Db    376  ValIleGlyLysMetGluArgGluAspIleGluSerLeuLeuLysTrpGluValGlyTrpLeu  395

Qy    1198 CAGGAGCTGGCCCCCGACTGGAGACTCCCTACTGGTGGGCCGCCAGCTGA  1257
           ||||||||||||
Db    396  HisGluLeuLeuGlyLysArgGluGlnSerProTyrTyr  407

Qy    1258 GGGAACAGCTCCGGGCACCCGCCTCGGCCTACAGCACGCAGCGACGCAGCGGGG  1317
           |||||||||
Db    408  GlyAsnAsnThr---  411

Qy    1318 CTGGAGCTGCTGGGCGGCGCCGGCCTGCCGGCCTACTCCCTCTACTTCGCA  1377
           |||||||||||||
Db    412  ------------LeuGlyGlyProSerIleArgSerAlaTyrIleLeuAlaLeuTyrPheThr  428

Qy    1378 CTCAGCAGCCTCACCACGGGCTTCGGCCAACGTGTCGCCCACACGGACACCGAGAAG  1437
           |||||||||
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Db    429  LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspAlaGluLys  448

Qy    1438 ATCTTCTCCATCTGCACCATGCTCACCATGCTCATCGGCGGCCTGGTGCTGGGGAAC  1497
           |||||||||||||||
Db    449  IlePheSerIleCysThrMetLeuThrMetLeuIleGlyGlyLeuValLeuGlyAsn  468

Qy    1498 GTGACGGCCCATCACTCCCAGCATGTACCCCGGGCCTTTCTGTACCACAGCGCCACGCGC  1557
           |||||||||||
Db    469  ValThrAlaHisHisSerGlnHisValProArgAlaPheLeuTyrHisSerAlaThrArg  488

Qy    1558 GACCTCCGGACTACAATCCCGCATCCACCGGTACCCCAAAGCAGCACGGTCACGG  1617
           |||||||||||
Db    489  AspLeuArgLeuAspPhePheIleProHisProProLysGlnGln  508

Qy    1618 GAGTACTTCCAGGCCACCACCTGGGCGTGGGTGAACAATGGCATTGGCATGCGCGG  1677
           ||||||||||
Db    509  GluTyrPheGlnAlaThrThrTrpProValAsnAsnGlyIleGlyMetArgArgLys  528

Qy    1678 AGCCTCCCTGACGAGGTGCCGCCAGACACATGGCCATGCCACGGTGCCGCTGCAG  1737
           |||||||||||||
Db    529  AspPheProAspGluGluProSerArgAspIlePheThrMetHisLeuGlnLeuLeuGln  548

Qy    1738 CTGCCACTGTTTGAGGGCGGCCAGCCGCCGGGCGGGCGGGCACTGTCTCTGCCCATCCTA  1797
           |||||||||||
Db    549  LeuSerLeuPheGluCysAlaSerArgGlyCysLeuArgSerLeuSerLeuHisIleLys  568

Qy    1798 CCCGCCCTTCGCACGCCCGGGGTACCCATCATCCCCGGGAGCTGGAAGGGCCAAT  1857
           ||||||||||||
Db    569  TyrPheValCysSerGlyValLeuValLeuGlySerMetGluValLeuLeuAlaIleLeu  588

Qy    1858 TACTTTGTCTGCTCTGGCTCCATGGAGGTGCTCCTGGCCATCCTA  1917
           |||||||||||
Db    589  GlyLysGlyAspProLeuIleLeuGlyAlaAsnLeuSerIleLeuLysThrAsn  608

Qy    1918 GGGAAGGGCGACCTGATCGGGCTGGTACCCGGAGTGCCCCGGGAGCAGGTGGTGCCCAAT  1977
           ||||||||||||
Db    609  GlyLysGlyAspLeuIleGlyLeuAlaAsnLeuSerIleLeuLysThrAsn  628

Qy    1978 GCCCAGCGTGAAGGGCCTGACGTACTGCGTCGCTGCTGCACGGTCGGCCGCGCAC  2037
           |||||||||||||
Db    629  AlaAspValLysLeuAlaLeuThrTyrCysAspLeuGlnLysLysLysGlyLeuPhe  648

Qy    2038 GACAGCCTTGCGCGTGTACCCCGGAGTTGCCCCGGCCTTCAGTCGTGGGCCTG  2097
           :: |||
Db    649  GluValValLeuAspLeuTyrProGlyTyrArgAlaHisLysPheValGluGlnHisAsp  668

Qy    2098 CTCAGCTACAACATGCTGGGTGCTGGG  2130
           ||||||||||||
Db    669  LeuGlnThrTyrAsnLeuValGlyHisGluSerArgLeuSerArgAsnLys  688

Qy    2131 GCAGAGGTGGACACCAGCTCCCTGAGCGGGCGACAATACCCTTATCTGCAGGCTG  2184
           ||||||||||
Db    689  SerMetValSerGlnSerGluProLysGlyLysAsnIleAsnLysArgLeuProSer  708

Qy    2185 ------GAGGAAGGAGAGAGACAGATGGGAGGACGGGCCCCCACGGGTCTCCCAGCC  2232
           :::
Db    709  IleValGluAspGluGluGluGluGluGluGluGlyGluGluGlyAlaValAlaSer---  726

Qy    2233 CCAGCTGATGAGCCCTTCCACGCTCGTCCCCTGGCTG  2292
           |||||||||||
Db    727  ------------LeuSerProIleCysThrArgGlySerSer  737

Qy    2293 GCCAAGCTGCTATCCCCACGTCGAACAGCACCCCGGGGAGCTGGGGAGGGAG  2352
           :::
Db    738  ------  738

Qy    2353 CCAGGCAGGGGCAGGGCTTTGAAGGCTGAGCCTGGCCCCTCTGCT  2397
           |||||||||||
Db    739  AsnLysLysValGlySerAsnLysSerAlaTyrLeuGlyLeuSerLeuLysGlnLeuAlaSer  758

Qy    2397 ------  2397
Db       ------  2397
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RESULT 5
088877
ID   088877    PRELIMINARY;    PRT;  1102 AA.
AC   088877;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Potassium channel.
GN   ELK1.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98382545; PubMed=9714851;
RA   Shi W., Wang H.S., Pan Z., Wymore R.S., Cohen I.S., McKinnon D.,
RA   Dixon J.E.;
RT   "Cloning of a mammalian elk potassium channel gene and EAG mRNA
RT   distribution in rat sympathetic ganglia.";
RL   J. Physiol. (Lond) 511:675-682(1998).
     EMBL; AF061957; AAC15520.1; -.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_nlg.
DR   InterPro; IPR000636; M+channel_pore.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM00086; PAC; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS00042; CNMP_BINDING_3; 1.
KW   Ionic channel.
SQ   SEQUENCE 1102 AA; 123230 MW; A135CC36E27F1A3 CRC64;

US-09-965-830-1_copy_6_3257 (1-3252) x 088877 (1-1102)

Alignment Scores:
Pred. No.:               1
Score:                   8.36e-132            Length:        1102
Percent Similarity:      62.00%               Matches:       551
Best Local Similarity:   48.80%               Conservative:  149
Query Match:             41.30%               Mismatches:    295
                         11                   Indels:        134
                                              Gaps:          24
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Qy    1 ATGCCGGCCATGCGGGGGGCGGCCTCCTGGGCGGCCTCAGAACACCTTCCTGGACACCATCGCTACG 60
          ||||||   ||||:::||||||| |||  ||||||||| |||::|||  ||:::|||||||||||
Db    1 MetProValMetLysGlyLeuLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy   61 CGCTTCGACGGACACGACAGTAACTTGTGCGTGGGCAACGCCCCAGGTGGCGGGCGGTCTTTC 120
          ||||||   ||||  |||||||||||||:||:|| |||||||||||||| |||| ||||
Db   21 ArgPheAspGlyThrHisSerAsnPheIleLeuAlaAsnAlaGlnLysGlyGlyGlyArgSerPhe 40

Qy  121 CCCGTGGTCTTACTGGCTGTCTGATGGCCTTCTGTGTGACCTCACGGGGGGGCTTGAGTC 180
          |||||||  ::::|||||| ||||||||||||||||||||||||||||||||  |||||
Db   41 ProLeuValTyrCysSerSerAspGlyPheCysSerGluAsnGlyAlaArgGlnAlaArgThrGluGluVal 60

Qy  181 ATGCAGCGCGGGGCTGTGGTGGCCTGCTCCTCCTTCCTTTATGGGGCCGAGCAGCTGGCCACGCCGGCCTG 240
          ||||||||| |||| |||||||| ||||||| ||:::||::|| |||||| ||:::||||||||:::|||
Db   61 MetGlnLysGlyCysGlySerCysAspAspSerProHisLeuLeuValGluThrArgAsnGluLeuMet 80

Qy  241 CAACAGATCCCGGAAGGCCCCTGGACGACGAGCACAAGGAGTTCAAGGGTGAGGCTC 300
          ||||| |:::|||||||||||||||| |||||||||||||||||||||  |||:::
Db   81 LeuGlnIleGluLysSerLeuLeuGluLysValGluPheLysGlyGluMetPheTyr 100

Qy  301 CGGAAGAGCGGGCGCTCCCGGTTCGTTGGGTGTCTCCTGGAGGTGATACCCATAAAAGAGAAA 360
          ::::|||:::||| ||||||| |||||||||||||||||||||:|||||||||||:::|||
Db  101 LysLysAsnGlyAlaProPhePheCysSerLeuLeuAspIleValProIleLysLysAsnGlyLys 120

Qy  361 GGGGAGGTGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAGAACCGA--- 417
          |||:::||:|  |||||||||  ||||||||||||||:::||||||||||||||||||  :::
Db  121 GlyAspProValValLeuPheLeuAlaSerPheLysAspIleThrAspThrLysValLysIle 140
```

```
Db  759 GlyThrValProPheHisSerProIleArgValSerArgSerAsnSerProLysThrLys 778
Qy 2398 ------------CCCCA------------------------ 2398

Db  779 GlnIleLeuAspProAsnHisAsnLysArgLysGlyAsnLeuGlnLeu 798
          |||                                     :::          |||:::||||
Qy 2434 ATGCCATTGGAAT--------GTGCCCCCAGATCTGAGCCCCAGGGTAGTAGGCCATTGAA 2487

Db  799 SerThrLeuAsnAsnAlaGlyGlyProProAspLeuSerProArgIleValAspGlyIleGlu 818
Qy 2488 GACGGCGTGGGTCTGGGACCAGCCCAAG---TTCTCTTTCGGCGGCTGGGCCCAGCTGTCGGCCG 2544

Db  819 AspGlyAsnSerSerGlyGluSerGlnThrPheAspPheGlySerGluArgIleArgSer 838
          |||                  :::||| :::        :::
Qy 2545 GAATGTAGCAGCAGCACCCCTCCCCTGGA---CCAGAGACGGCGGCCTGCTCACTGTTCCCCAT 2601

Db  839 GluProArgIleSerProProLeuGlyAspProGluIleGlyAlaAlaAlaValLeuPheIle 858
          |||:::|||                                  :::
Qy 2602 GGGCCGACGGAGGCAAGGACACAGACGACACTGACAAGCTTCGGACAGGCGGTGACAGAG 2661

Db  859 LysAlaGluGluThrLys------GlnGlnIleAsnLysSerLeuAsnSerGlnValThrThr 876
          |||||||:::||||||                    :::
Qy 2662 CTGTCAGAGACGGTGCTGCAGAATGCGGGAAGGACTCACAGTCACTTCGCCAGCCGTGCAG 2721

Db  877 LeuThrGlnGlnValSerGlnLeuGlyLeuLeuLysAspMetArgAsnValIleArgLeuLeuGlu 896
          |||:::|||||                      :::
Qy 2722 CTTTGTTCCTTGCGCCC--------------------- 2754

Db  897 AsnValLeuSerProGlnGlnProSerArgPheCysSerLeuHisSerThrSerValCys 916
          |||||||:::|||
Qy 2755 CCTCGGGCA------------------------------- 2787

Db  917 ProSerArgGluSerArgGlnThrArgThrSerProSerAlaHisGlnProCys------ 934
          |||                                  :::||| |||
Qy 2788 AGCACCTCCGGGCTTCTGCAGCCTCTGTGTGTGGACACTGGGGGCATCCTCCTACTGC--- 2844

Db  935 ------LeuHisLeuGlnThrGlyGlyAlaAlaTyrThrGln 946
          |||||| |||:::||||||||  |||:::||||||
Qy 2845 CTTGCAGACCCCCAGCTGGCTCTGTCTTGTTGGGCACTTGGGGACTTGGGGCGGGGCCT 2904

Db  947 AlaGlnLeuCysSerSerAsnIleThrSerAspIleThrTrpSer 960
          |||                          :::               |||
Qy 2905 CCTCCCCCTCATTGGACACCCTGCCCTGGGGGTCGGGGGTGTCCAGAGCCTCCCCCTGGCCT 2964

Db  961 ------ValAspProSerSerValGlySerSer---Pro 970
          |||||||||||||:::||||                  |||
Qy 2965 CGAGCCACAGCTTTCTTGGACCTCCACACTCAGAGCCCCTGCCCTCAGGAGACCTC 3024

Db  971 GlnArgThrGly------AlaHisGlyGlnAsnProAlaAspSerGluLeu 985
          |||:::                    |||||||   :::|||
Qy 3025 TGCTCTGAGCCCACCACACCCCTGCCTCCCCT------ 3054

Db  986 TyrHisSerProSerLeuAspThrTyrSerProSerHisSerThrTyrGlnValValGlyHis 1005
          :::                                  |||
Qy 3055 ------CCTCCTTCTGAGGAAGGGCCTAGGACTGGGCGCCCAGAG 3093

Db 1006 LeuGlnPheLeuArgCysIleSerProHisSerAspSerThrLeuThr---ProLeuGln 1024
          |||||||                          :::              |||
Qy 3094 CCTGTGAGCCAGGCTACCAGCACTGGAGAGCCCCACAGGGGCGTCAGGGGGCCTG 3153

Db 1025 SerIleSerAlaThrLeuCysSerSerSerValCysSerSerAsnIleThrSerLeuHisLeu 1044
          :::|||                                     |||
Qy 3154 GCCTTGCCCTGGGACCCCCACCCCTGGAGATGGTGCTTATTGGCTGCGTGGGCTTCTGGC 3213

Db 1045 ValLeuPro------SerArgSerGluGlu 1058
          |||     |||||||   |||
Qy 3214 ACAGTC------CAGTGGACCCAGGAA 3234

Db 1059 ThrValSerSerPheSerLeuGluAsnLeuProGlySerTrpAsnGlnGlu 1075
          |||||||                            :::
```

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Qy    418  GGGGGCCCGCACAGATGGAGGAGACAGGTGGTGGCCGGCCCGGCACGA 477
           |||::|||||   ||| |||||||||||||||||||||||||||||||
Db    141  ThrSerGluAspLysLysGluAspArgAlaLysGlyArgSerArgAlaGly------ 157

Qy    478  TCCAAAGGCTTCAATGCCAACCGGCGGGCGGGCGGTGCTTCTACCACCTGTCCGGG 537
           |||   |||||||||||||::|||   ||| ||||||||||||||||||:::|||
Db    158  ---SerHisPheAspSerAlaAlaArgArgArgAlaValLeuTyrHisIleSerGly 176

Qy    538  CACCTGCAGAGCACGCCAAGGGCACAGAGCCAATAAGGAGGTGGTTGGGGAGAAA 597
           |||   ::|||                     ||| |||   ::|||
Db    177  HisLeuGlnArgArgThrGluTyrLysGlyLysIleAsnAsnValPheValAspLys 196

Qy    598  CCAAAACTTGGCTGACTACAAAAGTAGCGCCATCCGGAAGTCGCCCTTCATCCTGTTGCAC 657
           |||||| ||||||||::|||   :||||||||||||||:|||||||||||
Db    197  ProAlaPheProGluTyrLysValSerAspAlaAlaValLeuTyrHisIleLeuHis 216

Qy    658  TGTGGGGCACTGAGAGCCACCTGGGATGGCTTCAATGCCAACCGGCGGGTGTTGGGGGAA 717
           :||||||||||||||||| |||||::|||
Db    217  PheSerThrPheLysAlaGlyThrAspTrpLeuIleLeuLeuAlaThrPheTyrValAla 236

Qy    718  GTCACTGTGCCCTACACAGGTGGTGTTGTGAGCACAGACAGGGAGCCCAGTGCGCGCGGC 777
           |||   ::|||                    ||| |||   :::||
Db    237  ValThrValProTyrAsnValCysPheIleGlyAsnGluAspLeuSerThrThrArgSer 256

Qy    778  CCGCCCAGGTGTCGACCGGCCGTGAGGTGCGCGTTCATCCTTGACATTGTGCTGAAT 837
           |||||||||:||::|||   ||||||||||||||||::|||
Db    257  ---ThrThrValSerAspIleAlaValIleLeuGluPheIleIleLeuLeuAsn 275

Qy    838  TTCCGGTACCACATTCGTGTCCAAGTCGGGCAGGTGGTGTTTGGCCCCAAAGTCCATTGC 897
           |||::|||                    ||| |||   :||
Db    276  PheAsnArgThrThrTyrValSerLysSerGlyGlnValIleValIleLeuLysThrSerSerCys 295

Qy    898  CTCCACTACGTCACCACCTGGTTCTCGCGACGCGTGCCCTTTGACCTG 957
           ::||||||||||||||||:|||   ||||||
Db    296  IleHisTyrValThrThrTrpPheIleIleAspLeuLeuAlaLeuProPheAspLeuAsn 315

Qy    958  CTACAGCCCTTCAAAGTGTACTTCGGGGACATGGTGGCCTGGAACACGGGTTGGCGCCTG 1017
           |||   ::|||                    ||| |||
Db    316  LeuThrLeuLeuMetSerMetPheAlaLeuGluLeuAlaHisTrpMetAlaCysIleTrpTyr 335

Qy   1018  CTGGCCATGCTGGGACGGGTTACTCCGGCGCTGCCGGTGACC 1077
           ::||||||||||||||||:||   ||||||
Db    336  LeuArgLeuLeuLeuGlnLysLeuAspArgTyrSerGlnHisSerThrHisIleVal 355

Qy   1078  CTGACACTGCTCANGGCCGTGTTCGCCCTGCCTGCCGCTGCCGCTGG 1137
           ::||||||||||||||||:||   ||||||
Db    356  LeuThrLeuLeuMetSerMetPheAlaLeuGluLeuAlaHisTrpMetAlaCysIleTrpTyr 375

Qy   1138  TACATTGGCCACGGGGAGATCGAGAGCAGGAATCCGACTTGCTGGCTG 1197
           ::|||                    :::|||||
Db    376  ValIleGlyLysMetGlyArgGluAspAsnSerLeuLeuLysTrpGluValGlyTrpLeu 395

Qy   1198  CAGGAGCTGGCCGCCCGACTGGGAGACTCCCGGTCGGGCCGAGGCCAGCTGGA 1257
           :::||||||||||||||||||:||   ||||||
Db    396  HisGluLeuGlyLysLysArgLeuGluSerProTyrTyr------ 407

Qy   1258  GGGAACAGCTCCGGCACAGAGTGACAACTCAGCAGCGAGCCAACGGGGACGGGG 1317
           ||||||||||||||||||||||||:||   ||||||
Db    408  GlyAsnAsnThr------------ 411

Qy   1318  CTGGAGCTTGCTGGGCGCCGGCCTACGCGCCCTACACCTCCCCTCTCGCA 1377
           |||||:||                    ||| |||
Db    412  -------LeuGlyGlyProSerIleArgSerAlaTyrIleAlaAlaLeuTyrPheThr 428

Qy   1378  CTCAGCAGCCTCACCACGCTGGGCCGGCCAACCGTGTCCGGCAACGACGAGAAG 1437
           |||||||||||||||:||||||   ||||||
Db    429  LeuSerSerLeuThrSerValGlyPheGlyAsnValSerAlaAsnThrAspLaaGluLys 448

Qy   1438  ATCTTCTTCCATCTGCACCATGCTCATCGGCACGGGCCTGGTGTTGGGAAC 1497
           |||||||||||:||||||   ||||||
Db    449  IlePheSerIleCysThrMetLeuIleGlyThrGlyLeuValPheGlyAsn 468

Qy   1498  GTGACGGCCATCACCAGCGCATGTACGCCCCGCGCCTTTCTGTACCACACCGCACGCGCC 1557
           ::|||                    ::||||||
Db    469  ValThrAlaIleIleLeuGlnArgMetTyrSerArgTrpSerLeuTyrHisThrArgThrLys 488
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RESULT 6
Q9UD05

ID   Q9UD05      PRELIMINARY;     PRT;    1017 AA.
AC   Q9UD05;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   BEC2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99386988; PubMed=10455180;
RA   Miyake A., Mochizuki S., Yokoi H.; Kohda M., Furuichi K.;
RT   "New ether-a-go-go K+ channel family members localized in human
RT   telencephalon.";
RL   J. Biol. Chem. 274:25018-25025(1999).
DR   EMBL; AB022698; BAA83592.1; -.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR006636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50042; cNMP_BINDING_3; 1.
DR   PROSITE; PS50112; PAS; 1.
SQ   SEQUENCE   1017 AA;  111693 MW;  4B480DFC75816A38 CRC64;

Alignment Scores:
Pred. No.:
Score:                7.71e-129       Length:            1017
Percent Similarity:   2461.50         Matches:            538
Percent Identity:     59.19%          Conservative:       119
Best Local Similarity: 48.47%         Mismatches:         245
Query Match:          40.43%          Indels:             208
DB:                   4               Gaps:                23
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us-09-965-830-1_copy_6_3257 (1-3252) x Q9UD05 (1-1017)

Qy      1 ATGGCGGCCAATGCGGGGCCTCCTGGCGTCCTCAGAACACCTTCCTGGACAACCATGGCTACG    60
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MetProValMetLysGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr    20

Qy     61 CCGCTCGGTCTACTGCTCTCGATGGCGTTCGTGACCATCAGCGGGGGGGGGTCTTCCCCGAGGTC   120
          |||||||||||||||||||||||||||||||||||||||  |||  |||||||||||||
Db     21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaGlnAsnThrPheLeuAspThrIleAlaThr    40

Qy    121 CCCGTGGTCTACTGCTCTCGATGGCGTTCGTGACCATCAGCGGGGGGGGGGTCTTCCCCGAGGTC  180
          |:||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db     41 ProIleValTyrCysSerAspPheLeuLeuAlaGlnAsnThrPheLeuAspThrIleAlaThrArgGluVal    60

Qy    181 ATGGCAGCGGGGGCGTGTGCCTGCTCCTTCCTTATGGGGCGCAGACACCAGTGAGCTCGTCCGC  240
          |||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 MetGlnLysThrCysSerCysArgPheLeuTyrGlyProGluThrSerGluProAlaLeu    80

Qy    241 CAACAGATCCGCAAGGGCCCTGGACGGACGCACAAGGAGTTCAAGGCTGATGATCCTGTAC  300
          ||:::||  |||||||||||||||||||||||||||||||||||||||||||||||||||
Db     81 GlnArgLeuHisLysAlaLeuGluGlyHisGlnHisGlyAlaGluIleIleCysPheTyr   100

Qy    301 CGGAAGAGCGGGCTCCGGAGCACCGCTCCCCCGTTCTCGCCCGGATGTGATACCATAAAGAATGAGAAA  360
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    101 ArgLysAspGlySerAlaAlaPheThrProCysSerLeuLeuAspMetMetProIleLysAsnGluMet  120

Qy    361 GGGGAGGTGGGCTCTTCCTTCCTAGTTCTCACAAGGACATCAGCAAACAAAGAACCGAGGG  420
          |||||||||||||||||||||||||||||||||  |||::|::||||||||  :::
Db    121 GlyGluValValLeuPheLeuProHeSerPheLeuAspSerProThrGlnSerGlySerProGly   140

Qy    421 ---GGCCCCGACAGATGGAAGAGAGACAGGTGGTGGGCCGCGGCGACTAGCGCCGGGCACGA   477
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    141 LeuGlyProGln---------------------GlyGlyArgGlyAspSerAsnHisGluAsn   154

Qy    478 TCCAAAGGC--------------------TTCAATGCCAACCGGCGGGGGGGGGGAGCCGGCGGGGCC   516
          ||||||||                      ||||::|||||||||||||||||||||||||||
Db    155 SerLeuGlyArgGlyAlaThrThrLysPheArgSerArgAlaArgAlaArgArgSerArgThr   174

Qy    517 GTGGCTCTACCACCTGTCCGGGGACCTCCAGAGAGCACGGCCAAGGACACACAAGGCTCAAT  576
          |||||||:::|||||||::|||||||||||||||||||||||||||||:||||||||:||
Db    175 ValLeuHisArgLeuThrGlyHisPheGlyArgArgGlyLeuGlyMetLysAlaLeuAsn   194

Qy    577 AAGGGGGTGTTTTGGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCGGCCGAAG   636
          |||||||||:::||||||||||||||||:|:::||||||||||||||||:|||
Db    195 AsnAsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGly   214

Qy    637 TCGCCCTTCATCCTGTTGCACTGTGGGCACTGAGAGCCACTGGGATGGCTTCATCCTG   696
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          Db    825 GluThrGlnThrPheAspPheGlySerGluGlnIleArgProGluProArgIleSerProGlu   844
Qy    2563 TCCCCTGGACCAGAG-------AGGGGCCTGCTCACTGTTCCCACATGGGGCCCAGCGAG  2613
           |||                  :::
Db    845 SerLeuGlyGluSerGluIleGlyAlaAlaPheLeuPheIle-----------Lys   859

Qy    2614 GCAAGGAACACA---GACACACTGGACAACGCTTCGGCAGGCGGGGTGACAGAGCTGTCAAGAG   2670
           ||| |||           |::::
Db    860 AlaLeuGluThrLysGlnIleIleAsnLysLeuAsnSerGluvalThrPheLeuThrGln   879

Qy    2671 CAGGTGCTGCAGATGGGGGAAGGAACGACTACAGTCAGCCCAGGCGTTGTGCAGCCAGG  2730
           ||||:|::||||||||||||     ||:||| :::||
Db    880 GluValSerGlnLeuGlyLysAspMetArgSerIleMetGlnLeuLeuLeuGluAsnIleLeu   899

Qy    2731 GCGGCCCACAGGGAGGGTCCGTGCCTCGGCGCATCGGGAGAGGGGGGCCGTTGCCCAGCCAGC  2790
           :::||:|||               ||| ||| :::||| :::|
Db    900 SerProGlnGlnProSerGlnPheCysSerLeuHisProThrProSerIleCysProSerArg   919

Qy    2791 ACCTCCGGGCGTTCTCGACCGCTTCTGTGTGTGGACACTGGGCCATCCTCCTACTGCCCTGCAG  2850
           :::
Db    920 GluSerPheGlnThrArg--------ValSerTrpSerAlaHisGlnProCysLeuHis   936

Qy    2851 CCCCCAGCT-------------------GGCTCTTGTCTTGAGTGGGACTTGGCCCCAC   2889
           ||||| |                     ||||:::|||
Db    937 LeuGluIleAlaAsnGlyAlaHisLeuTyrHisGlyAsnValThrSerAspIleTrp-------   954

Qy    2890 CCTCGTCCGGGGCGCCTCCTCCCTCAWGGCACCGGGTCCCCAGCGGTCTCAG  2949
           ||| |||||||||||||||||||||||||||||||||||||||||||||||||  :::
Db    955 ------SerValAspProSerLeuValGlyLysAsnProGlnArgThrGluAlaHisGlu   972

Qy    2950 AGCTCCCCC-------------------------------TGGCCTCGAGCCACA   2973
           |||||
Db    973 GlnSerProValAspSerGluHisHisSerProAsnLeuAlaTyrSerProSerHis   992

Qy    2974 GCTTTTCTGGACCTCCACCTCAGACTCAGAGCCCCCTGCCCTTGGCTGGTTGCTGAGTC  3033
           |||||||||||||||||||||||||||||||||||||::||||||||||||
Db    993 CysGlnValIleGlnLeuGlyHisLeuGlnPheLeuUArgCysIleSerSerProHisSerAsp  1012

Qy    3034 CCCAGCACCCCT------------GGCTCCCCGTCCTCCTTCTGAGGAAGGGGTCTAGGACT---  3081
           |||
Db    1013 ThrThrLeuThrProLeuGlnSerIleSerAlaThrHisLeuSerSerSerValCysSerSer  1032

Qy    3082 GGGCCCGCAGAGCCTGTGAGCCAGGCTACCAGCACTGGAGAGCCCCCACCAGG  3141
           |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1033 SerGluThrSerLeuHisLeuValLeuProSerArgSerGlyLeuGlySerIleThrHis  1052

Qy    3142 TCAGGGGGCCTGGCCTTGCCTGGGAC  3168
           |||||||||||||||||
Db    1053 GlyProValSerSerPheSerLeu-----------------GluAsnLeuProGly  1065

Qy    1066 Ser-------------------TrpAspp  1068
```

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Db  215 |||||||||||| :||||||||||||                                    234
        SerArgCysLeuLeuHisTyrSerValSerLysAlaIleTrpAspGlyLeuLeu
Qy  697 CTCGGCACACTCTATGTGGCGTTCACTCACGGTGTCCCTACAGCGTGTGTGTGAGCACAGACACGG  756
        |||||||||||| :|||||||||||||

Db  235 LeuAlaThrPheTyrValAlaValThrHisValProTyrAsnValCysPheSerGlyAspAsp    254
        CGAGCCGCAGTGCCGCCCCCGGCCCCCCGGCCCCCCCAGCGTGTGACCTGGGAGGGTCCTCTTC  816
Qy  757

Db  255 AspThrProIleThrSerArgHisThrLeuValSerAspIleAlaValGluMetLeuPhe     274
Qy  817 ATCCTTGACATTGTGTGAAATTTCCGTACCACCATTCTGTTGCCAAGTGGGGCCAGGTGGTG     876

Db  275 IleLeuAspIleArgThrArgThrThrTyrValSerGlnSerGlyGlnValIle          294
Qy  877 TTTGGCCCCAAGTCCATTTGCCCACTACGTCCACCACTGGTTCTCCGGATGATCATC        936

Db  295 SerAlaProArgSerIleGlyLeuHisTyrLeuAlaThrTrpPheHisIleAspLeuIle     314
Qy  937 GCAGCGCGCCGTTTGACCTGCTACACATGTCAAGGTCATTCACTTCGGGAGCCAT         996

Db  315 AlaAlaLeuProPheAspLeuTyrIlePheAsnIleThrValThrSerLeuValHis       334
Qy  997 CTGCTGAGACGGTGCGGCCTGCTCGCCGGCCTTCCGCGGCGCTGGACCGGTAC          1056

Db  335 LeuLeuLysThrValArgGlyLeuLeuLeuArgLeuGlnLysLeuGlyArgTyr          354
Qy 1057 TCGGCTCGGCCTGCCGGTGTGCTGACACGTGGGCGTGTTCGCCCTGCTTCGCGGAC        1116

Db  355 SerGlnCysSerAlaValAlaValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHis  374
Qy 1117 TGGGTCGGCCTGCCTGGTTTTACATTGGCAGCGAGAGTCCAGAACGGAATCCAG         1176

Db  375 TrpMetAlaCysIleTrpThrTyrValIleGlyTyrArgGluMetGluAlaAsnAspProLeu  394
Qy 1177 CTGCCTGAGATTGGCTGGACTCGCAGGAGGTGGCCCCGCCCGACTCCTACTACTG        1236

Db  395 LeuTrpAspIleGlyTyrTrpLeuHisGluLeuGlyLysArgLeuUalValProTyr       412
Qy 1237 GTGGGGCCGGAGCCCAGCTGGAGGAACAGCTCCGGCACAGTGAACAACTGCCAGCAGC      1296

Db  412                                                                   412

Db  413 ValAsnGlySer                                                      426
Qy 1297 AGGGAGGCCAACGGGGAACGGGGGGCCTGGGAGCTGCTGCCCAGGCCCTAC             1356

Db  447 AlaAsnThrAspAlaGlyLysIlePheSerIleCysThrMetLeuIleGlyAlaLeuMet     466
Qy 1417 GCCAACACGGACGCCGGAAAGAATCTTCTCCATCTGCACCATGCTCATCGGGGCCCTGATG    1476

Db  467 HisAlaValAlaValProGlyAsnValThrAlaIleIleGlnArgMetTyrSerArgArgSer  486
Qy 1477 CACGCGGTGGTGTTTGGGAACGTGACGGCCATCATCCAGCGTATGAGCCGGCGCTTT       1536

Db  487 LeuTyrHisSerArgMetLysAspLeuLysAspPheIleAlaArgGlnProArg          506
Qy 1537 CTGTACCACAGCCGCGACTGGGAGTACTTCCAGGGACCAGAGGCATGGCAC            1596

Db  507 ProLeuLysGlnArgMetLeuGluTyrPheGlnThrThrArgAlaValAsnSerGlyIle     526
Qy 1597 CCCCTCAAGCAGCGCATGCTGGAGTACTTCCAGGCCGTGAACAATGGCAT             1656

Db  527 AspAlaAsnGluLeuLeuArgAspPheProAspGluLeuArgAlaAspIleAlaMetHis     546
Qy 1657 GACACCGACGAGCTGCTGCGAGAGCGCCGGAGCCAGACATCGCACGCAC              1716

Qy 1717 CTGCACAAGGAGGTCCTGCAGCTCCCCACTGTTTGAGGCGGCTGCTGCGG             1776


Db  547 LeuAsnArgGluIleLeuGlnLeuProLeuProHisGlyAlaAlaSerArgGlyCysLeuArg  566
Qy 1777 GCACTGTCTCGGCGTCGGGCGGCCTTCGCACGGCGGGGAGGTAGCTCATCCACCA        1836

Db  567 AlaLeuSerLeuHisIleLysThrSerPheCysAlaProGlyGluTyrLeuArgLeuArg     586
Qy 1837 GGCAGGATGCCCCTGCCAGGCCCTCTACTTTGTCTGCCTGCCTCCATGGAGGTCTCAAGGGT 1896

Db  587 GlyAspAlaLeuGlnAlaHisHisTyrTyrValCysSerGlyLeuValLeuArgAsp       606
Qy 1897 GGCACCGTGCTGCCATCCATCCTAGGGAGAAGGGCGGCACCTTGATCGTGCTGCCCGGCGG   1956

Db  607 AsnMetValLeuAlaIleLeuGlyLeuGlyAspLeuIleGlyAspIleProGlu          626
Qy 1957 GAGCAG                                                           1986

Db  627 GlyGlnGluProGlyLeuGlyValAlaAspProAsnPheValLeuLysThrSerAlaAspVal 646
Qy 1987 AAGGGGCTGACCTACTACGTCCTGCCTGGCAGTGTGTCGGACTGGCTGCCTGACACAGCCTT 2046

Db  647 LysAlaLeuThrTyrCysGlyTyrLeuGlnLeuGlnLeuSerGluArgGlyLeuAlaGluVal 666
Qy 2047 GCGGCTGTACCCCGAGTTTGCCCCGGCCGCTTCAGTCGGTCGTGGCCCGGAGGGAGGACTAC 2106

Db  667 ArgLeuTyrProGluTyrGlyValAlaAlaPheArgAlaGlyLeuProArgAspLeuThrPhe 686
Qy 2107 AACCTGGGTGCTGGGGGGCAGGCTCTGCGAGAGGTGGACACCAGCTCCTG             2154

Db  687 AsnLeuArgGlnGlySer                                                701
Qy 2155                                                                   2169

Db  702 ArgSerProArgLeuSerGlnProArgSerGluSerSerSerAspLysThr             721
Qy 2170 CTTATGTCCACGCTGGAGGAGAAGGAGACAGATGGGGACGCAGGGCCCCCA             2229

Db  722 LeuProSerIle                                                      734
Qy 2230 GCCCAGCTGATGAGGCCCTCCAGCCCCCCCGCTGTCCCGGCTGCCTCCTCATCCTCA       2289

Db  735 GlyIleGlyGlyProArgProArgArgProLeuProLeuProAsnLeuSerProAlaArgPro 754
Qy 2290 GCTGCCAAGCTG                                                     2301

Db  755 ArgGlySerLeuValSerLeuGlyGluGlnGluProProLeuGlyThrThrArgPheGlyPro 774
Qy 2302 CTATCCCCACGTCGAACAGCCACCCCGCCTCCTCAGGTGCCGCAGAGGGAG            2352

Db  775 SerProSerLeuSerProSerLeuSer                                      791
Qy 2353 CCAGGCAGGGCAGGGGGCTTTGAAGGCTGGCGCCCCTCTGCCTCCCACGGGGCCCTA       2412

Db  803 AlaAlaLeuAlaTrpLysProProGlyLeuLeuLeuIleLeuProProLeuGlyThrThrArgPheGlyPro 822
Qy 2413 GAGGGG                                                           2457

Db  823 LeuSerProArgIleValAspGlyIleSerGlyThrArgLeuAlaProSer            842
Qy 2458 CTGAGCCCCACGGGTAGTAGAAGGCAATTGAACAC---GGCTGTGGGGTCGGACCAGGCCCAAG 2514

Db  843 PheArgPhe                                                         859
Qy 2515 TTCTCCTTCCCGGTGGGCCAGTCTGGCCCGGAATGTAGCAGCGCCCCTCCCCTGACCA      2574

Db  860 ProThrGlyThrArgProSerProGluLeuAlaSerGluAlaSerGluGluValLysGluLys 879
Qy 2575 GAGAGCGGGCCGCCTCACTGTTCCCATGGGCCCAGCGAAGGACACA--GACACA          2631

Db  880 ValCysArgLeuAsnGlnGluValSerGlnLeu-SerAr                           899
Qy 2632 CTGGCACAAGCTTCGGCGACAGAGCAGGCGCTGCAGATGCTGCAGAAGAAATGCGGGGAA    2691
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RESULT 7
Q9R1I9

ID   Q9R1I9      PRELIMINARY;   PRT;   1017 AA.
AC   Q9R1I9;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   BEC2.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BRAIN;
RX   MEDLINE=99386988; PubMed=10455180;
RA   Miyake A., Mochizuki S., Yokoi H., Kohda M., Furuichi K.;
RT   "New ether-a-go-go K+ channel family members localized in human
RT   telencephalon.";
RL   J. Biol. Chem. 274:25018-25025(1999).
DR   EMBL; AB022699; BAA83593.1; -.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_binding.
DR   InterPro; IPR000636; M-channel_pore.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50042; cNMP_BINDING_3; 1.
SQ   SEQUENCE   1017 AA;  111403 MW;  BFDB0F1B35437C9F CRC64;
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Alignment Scores:
Pred. No.:
Score:            4.62e-128        Length:          1017
                  2447.50          Matches:         533
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Percent Similarity:   60.0%        Conservative:    131
Best Local Similarity: 48.24%      Mismatches:      243
Query Match:          40.20%       Indels:          198
DB:                   11           Gaps:            23
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us-09-965-830-1_copy_6_3257 (1-3252) x Q9R1I9 (1-1017)
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```
Qy    1000 CTGAAGACGGTGCGCCTGCTCTCGCCCTCGCTCCGGGGTTGGACCGGTACTCG 1059
           |||||||||||:::||||||||||||||||||||:||||||||||||||||||
Db     337 LeuLysThrValArgLeuLeuArgLeuLeuGlnLysLeuGluArgTyrSer    356

Db     317 AlaLeuProPheAspLeuLeuTyrValPheAsnIleThrValThrSerLeuValHisLeu 336

Qy    1060 CAGTACAGCGCCGTGGTGCTGACACTGCTCATGGCCGTGTTCGCCCTGCTCGGCCACTGG 1119
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     357 GlnCysSerAlaValValLeuThrLeuLeuMetSerValPheAlaLeuLeuAlaHisTrp 376

Qy    1120 GTCGGCCTGCTGTCGTTTTACATTGGCCAGGAATCCGAGCAGCGAGCAGCTG 1179
           ||||||||||||||||||||||||||||||||::||||||||||||||||||
Db     377 MetAlaCysValTrpTyrValIleGlyArgArgIleAlaAlaAspProLeuLeu 396

Qy    1180 CCTGACAATTGGCTGGCCACGCGACTGGAGGACTCCCTACTCGTG 1239
           ||||||||||||||||||||||||||||||||||||||||||
Db     397 TrpAspIleGlyTrpLeuHisGluGluGlyLysArgLeuGluProTyr        413

Qy    1240 GGCCGGAGGCCCAGCTGGAGGAACAGCTCCGGCGAGTGACAACTCGAGCAGC 1299

Qy    1300 GAGGCCAAACGGACGGGGCTGGGAGCGCTGCTGGGGCGGGCCGGCCTACATC 1359
Db     413
```

(Sequence alignment — Qy/Db rows continuing across the page, rotated layout)

```
Qy   3004 ------------------------------------------------------------ 3004
Db    951 rThrLeuAlaValValHisCysProAlaSerValGlyThrValGluIleGlyAlaThrPr  971

Qy   3005 ------------------CCCCTGCCTCAGGAGGACCCTGCTCTGAGCCC            3036
                             |||       |||         |||   ||
Db    971 oSerGluLeuArgSerSerMetValProProPheProSerGluProAspProLeuGlyPr   991

Qy   3037 AGGACCCTGCCT                                                 3049
          |:||:||||:|||
Db    991 oSerProValPro                                               995
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RESULT 8

O89048

SEQUENCE 8

Alignment Scores:
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Pred. No.:                 1.29e-127      Length:           1017
Score:                     2439.50        Matches:           532
Percent Similarity:        60.00%         Conservative:      131
Best Local Similarity:     48.14%         Mismatches:        244
Query Match:               40.06%         Indels:            198
DB:                        11             Gaps:               23
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US-09-965-830-1_COPY_6_3257 (1-3252) x O89048 (1-1017)

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Qy      1 ATGCCGGCCATGGGGGGGGCCTCCTGGCCGCCTCAGAACACCTTCCTGGACACCGGCTACG   60
          |||                 |::||||:||||:||
Db      1 MetProValMetLysGlyLeuLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr   20

Qy     61 CGCTTCGACGGCACGCACAGTACTACTTCGGTGGGCACGCCGAGGTGGCGGGGCTCTTC    120
          ||||:||||||||||||:::||||||
Db     21 ArgPheAspGlyThrHisSerAsnPheLeuLeuAlaAsnLeuGlnGlyProArgLeuProPhe   40

Qy    121 CCCGTGGTCTACTCCTCGATGGGTTTCGTGACCTCACGGGGGTCCCGGGCTGAGGTC     180
          |||:|||||||  ::|||||||:||||||||||:|||||||:||||||||::
Db     41 ProIleValTyrCysSerSerAspGlyPheGlyGluLeuThrGlyTyrGlyArgThrGluVal   60

Qy    181 ATGCAGCGCGGGGGCTGTGCCCGCTCCTTCTTTATGGGCCAGACCACCAGTGAGCTCGTCCGC  240
          |||::|||  :::||||
Db    413 ------------------------------------------------------------   413
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```
Db     61 MetGlnLysThrCysSerCysArgPheLeuThrTyrGlyProGluThrSerGluProAlaLeu   80
Qy    241 CAACAGGATCCCGCAAGGCCGGCCCTGGACGAGGAGCACCAAGGAGTTCAAGGCTGATCCTGTAC  300
          ||||:::||||||||||||||||||:::||
Db     81 GlnArgLeuGlnLysAlaLeuAlaLeuGlyHisGlnGluHisSerArgAlaGluIleCysPheTyr  100

Qy    301 CGGAGAGCGGCGGCCTCCGGTTCTTGGTGTCTTCCGGATGTGAATCCATAAAGAATGAGAA      360
          |||                 ||||||:::||
Db    101 ArgLysAspGlySerAlaPheTrpCysLeuLeuAspMetMetProIleLysAsnArgThrVal   120

Qy    361 GGGGAGGTGGCTCTCTTCCTAGTGTCTCACAAGGACATCAGGAGAACCAAGAAACCAGAGG     420
          |||                 ||||:::||
Db    121 GlyGluValValLeuPheLeuPheSerPheGlnSerGlyGly                      140

Qy    421 GGGGTGTTGGGGAGAAAAACAAACTTGCCTGAGTACAAAGTAGGCCGCCATCCGGAAGTCG    480
Db    141 LeuGlySerProGlyIleHisGlyAspAsnAsnHisGluAsnSerLeuGlyArg-         159

Qy    460 CGATANGGCCGGGGACACGATCCAAAAGGCTTCAAATGCCAACCGGGGGGGGGGGGCCGTG    519
Db    160 ------ArgGlyAlaSerSerArgLeuArgSerThrArgArgGlnAsnArgThrVal      176

Db    177 LeuHisIleArgLeuHisTyrHisSerProGluGlyArgArgAspGluGlySerValLysSer   196
Qy    520 CTCTACCACCTGTCCGGGCACCTGCAGAAGCAGCCCAAGGGCAAGCACACTCAATAAG      579

Qy    580 GGGGGTGTTTGGGGAGGAAAACAAACTTGCCTGAGTACAAAGTAGGCCGCCATCCGGAAGTCG    639
Db    197 AsnValPheGluProLysProSerValProGluTyrLysValAlaSerValGlyGlySer     216

Db    217 ArgCysLeuLeuLeuHisSerTyrSerIleProLysAlaValAlaValTrpIleLeuLeuLeu   236
Qy    640 CCCTTCATCCTGTTGCCACTGTGGGGGGCCACCGAGAGCGCACCGGCCTTCATCCTGCTC    699

Qy    700 GCCACACTCATGTGGCGTGGCTCACTGGCCCTACCACCGTGTCGTGTAGCACAGGAG       759
Db    237 AlaThrPheTyrValAlaValThrValProGlyTyrAsnValCysPheAlaGlyAspAsp    256

Db    257 ThrProIleThrSerArgHisThrLeuValSerArgIleAlaValGluMetLeuPheIle    276
Qy    760 CCCAGTGCCGCCCGGGGCGCCCCGCCAGGGTCTGTGCCGTGGAGGGTCCCTCTCATC      819

Qy    820 CTTGACATTGTGCTGAATTCCGTACCACATTCGTGTCCAAGTCGGGGCAGGTGGGTTT    879
Db    277 LeuAspPheIleLeuLeuAsnPheArgThrThrTyrValSerGlnSerGlyLeuValValSer  296

Db    297 AlaProArgSerIleGlyLeuHisTyrLeuAlaThrTrpPhePheValAspLeuIleAla    316
Qy    880 GCCCCAAAGTCCATTTGCCTCCACTACGTCACCACCTGGTTCCTGGTGGATCATCGCA     939

Qy    940 GCCGTGCCCTTTGACCTGCTACAAGCCTTCAACGTGACTTCGGGGGCCCCCATCTG      999
Db    317 AlaLeuProPheAspLeuLeuGlnTyrValPheAsnIleThrValHisThrSerLeuValHisLeu  336

Db    337 LeuLysThrValArgLeuLeuArgLeuLeuArgLeuGlnLysLeuGluArgTyrSer       356
Qy   1000 CTGAAGACGGTGCGGCTGCTGCGCCTGCTGCGGCTGCAGAAGCTGGAACGCTACTCG     1059

Qy   1060 CAGTACAACGCCGTGGTGCTGCTGCTGCTGCTCATGGGCGTGGTTCCCCCTGCCCACTGG    1119
Db    357 GlnCysSerSerAlaValValAlaLeuThrLeuLeuMetSerValProAlaLeuAlaHisTrp   376

Qy   1120 GTCGCGCCTGCGGTCTGGGTTTTACAATGGCCAGGAGATCGAGAGCAGGGAGAAATCCAGTG  1179
Db    377 MetAlaCysValTrpTyrValIleGlyArgArgGluMetGluAlaAsnAspProLeuLeu    396

Qy   1180 CCTGAGATTGGGTGGCTGCCAGAGACTGGACCCCGCGGGACTCCCTACTACCTGGTG      1239
Db    397 TrpAspIleGlyTrpLeuHisGluLeuGlyLysArgLeuGluGluProTyr------       413

Qy   1240 GGCCGGAGGCCAGCTGGAGGGAACACGCTCCGGCCAGAGTGACAACTGCAGCAGCAGC     1299
Db    413 ------------------------------------------------------------   413
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Qy  1300 GAGGCCAACGGACAGGGGCGGGCGCTGGGCGCTGGCTCGGGGCCAGGCGCCTACATC 1359
Db   414 ---ValAsnGlySerAla------------------GlyGlyProSerArgArgSerAlaTyrIle 428

Qy  1360 ACCTCCCTCTACTTCGGCACTTCAGCAGCCTGGGCGTTCCGCC 1419
Db   429 AlaAlaLeuTyrPheThrLeuSerSerLeuThrSerValGlyPheGlyAsnValCysAla 448

Qy  1420 AACACGGCACCGAGAAGATCTTCTCCACACTCTCCACCAATGCTCATCCGGCGCCCTGATCGAC 1479
Db   449 AsnThrAlaProArgIlePheSerIleLeuThrMetLeuIleGlyAlaLeuMetHis 468

Qy  1480 GCGGGTGGTGTTTCGGGAACGTGACGGCCAATCATCCAGCGCCATGTACGCCCGCGCCTTTCTG 1539
Db   469 AlaValValPheGlyAsnValThrAlaIleIleLeuGlnArgMetTyrSerArgArgSerLeu 488

Qy  1540 TACCACAGCCGCCACGCGCCGACCTACATCCCGGTATCCCCAAGCCC 1599
Db   489 TyrHisSerArgHisMetLysAspLeuArgValHisArgLeuProArgPro 508

Qy  1600 CTCAAGGACGGCCAATGCTGGAGTACTTCCAGGACCACCTGGGGGTGACAAATGGCATCGAC 1659
Db   509 LeuLysAspGlyArgMetLeuGluTyrPheGlnThrThrThrAlaValAsnSerGlyIleAsp 528

Qy  1660 ACCACCGAGCTGCTGCAGAGCCTCCCTGACGAGCTGCGCGGACGCGCGCCCTGCGCGGGCA 1719
Db   529 AlaAsnGluLeuLeuArgAspPheProAspGluLeuArgGlnAlaAlaMetHisLeu 548

Qy  1720 CACAAGGAGGTCCTGCAGCTGCCCACTGTTTTGAGGCGGCGCGGGGCGGGCATCCACGTATCCCCAAGCC 1779
Db   549 AsnArgGluIleLeuGlnLeuProLeuPheGlyAlaAlaSerArgGlyCysLeuArgAla 568

Qy  1780 CTGTCTCTGGCCCTGGCGCCGGCCGGCCGCGGGGGAGTACCTCATCCACCAAGGC 1839
Db   569 LeuSerLeuHisIleLysThrSerPheCysArgGlyProGlyPheLeuLeuArgGly 588

Qy  1840 GATGCCCTGCAGCGCCCTCACTTTGTCCTGCTCTGGCTCCATGGAGGTGCTGCTCAAGGGTGGC 1899
Db   589 AspAlaLeuGlnArgAlaHisPheValLeuLeuTrpLeuHisGlyGlyAlaAlaGlyAspAsn 608

Qy  1900 ACCGTGCTGCCCATCCTAGGGAAGGGCGACCTGATCGGCGTGTGAACCTGCCCCGGCGGGGAG 1959
Db   609 ThrValLeuAlaIleLeuGlyLysGlyAspLeuIleGlyAlaAspProGluProGluGly 628

Qy  1960 CAG------ 1995
Db   629 GlnGluProGlyAlaGlyAlaGlyValCysValLeuLysThrSerAlaLeuValLysSerAlaLeu 648

Qy  1996 ACGTACTGGGTCTCAGTGTCTGCAGCTGGCTGGCCCGCAGCCGTGCGTGGCTGTAC 2055
Db   649 ThrTyrTyrCysArgLeuGlnGlnLeuSerSerArgGlyLeuGluValLeuArgLeuTyr 668

Qy  2056 CCCGAGTTTGCCCCGCGGCTTCAGTGTGGTGCCTCCGAGGGAGCTCAGCTACAACCTGGGT 2115
Db   669 ProGluPheAlaProArgAlaLeuPheGluProArgLeuProArgLeuAsnLeuArg 688

Qy  2116 GCTGGGGGA---------- 2133
Db   689 GlnGlySerGluAsnAsnGlyLeuGlyArgPheSerProArgLeuSerGlnAla 708

Qy  2134 GAGGTGGACACCACCTCCCTGACAAATACCCTTAAGTCCACGCTGGAGGAGAAG 2193
Db   709 ArgSerAspThrLeuGlySerSerAspLysThrLeuProSerIle------- 725

Qy  2194 GAGACAGATGGGAGCAGAGGGCCCCACGGTCTCCCCAGCCTGATGAGCCCCTCCAGC 2253
Db   726 GluThrGlyGly----------GlyMetGluProGlyAlaGlySerLysProArgArg 741

Qy  2254 CCCCTGCTGTCCCCTGGCTCCACCTCTCATCCTCAGCTGCCAAGCTG--------- 2301
Db   742 ProLeuLeuLeuProAsnLeuSerProAlaArgProArgGlySerLeuValSerLeuLeuLeu 761
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Qy  2302 ------------------------------------------CTATCCCCACGTCGA 2316
Db   762 GlyGluGluLeuProProSerArgAlaLeuValValSerSerProSerLeuSerPro--- 779

Qy  2317 ACAGCACCCGGCCTCGTCTTAGGTGCAGAGGAGGCCAGGCAGGCAGGGGCTTTGAAG 2376
Db   780 ---ThrProSerProAlaLeuAlaGlyArgGly----- 789

Qy  2377 GCTGAGGCTGGCCCCTCT--------GCTCCCCCACGGGGCCCTAGGAGGG------- 2418
Db   790 ---SerSerProSerLeuHisGlyLysProProArgGlySerAlaAlaTrpLysProProPro 807

Qy  2419 ---CTACGGCGTGCCCCCATGCCATGGAAGTGCCCCCCAGAATTCTGAGCCCGCCTTGTCG 2475
Db   808 GlnLeuLeuThrProProLeuGlyTyrPheGlyProProAspLeuSerProTrpIleVal 827

Qy  2476 GATGGCATTGAAAGACGGGCGTGGC---TCGGACCAGCCCCAAGTTGTCTTTTCCGCGTGGGC 2532
Db   828 AspGlyIleGluGluAspSerSerAsnThrAlaGlyLeuAlaProThrPheArgPhe--- 844

Qy  2533 CAGTCTGCCCGGAAGTAGCAGCAGCCCCTCCCTGGACCAGGAGAGGGGGCCTGCTCACT 2592
Db   845 SerLysSerArgProGluProThrArgThrArgSerGlnAsnAlaProLeuSer------ 860

Qy  2593 GTTCCCCATGGGCCCCAGGCGGAGGCAAGGAAC------ACAGACACTGGACAAAGCTTCGG 2646
Db   861 --------GlyProArgLeuSerArgGluLeuLeuAlaLeuAlaThrGluGluValLys 877

Qy  2647 CAGGCGGTGACAGAGCTGTCAGAGCACCAGGTGCTGCAGATGCGGGAGGAGGACTGCCAGTCACTT 2706
Db   878 GluLysValCysArgLeuAsnGlnGluIleLeuSerArgLeuAsnGlnGluValSerGlnLeu 897

Qy  2707 CGCCAGGCGTGTCAGCTTGTCCTGGGCGCCCACAGGGAGGGTGCCCTGGGGATCG 2766
Db   898 SerArgGluLeuArgGlnValMet------ 905

Qy  2767 GGAGAGGGCGGGCCGTGCCCAGCCAGCACCTCCGGGGTCCGTGTCTTGTTGTCTGGGACTGGGCCC 2826
Db   906 ------GlyLeuLeuGlnAlaArg--- 911

Qy  2827 GGGGCATCCTCCTTACTCCCTGCAGCCCCCAGCTGGCCTCTGTGTTGAGTGGGGACTGGGCCC 2886
Db   912 ---LeuGlyProSer------ 916

Qy  2887 CACCCTCGTTCCGGGGGCCCTCCCCCCTCATGGCACCCTGGGCCTCCCCAGGGTCT 2946
Db   917 HisPro-------ProAsp-SerThrTrpLeuProAspLeuProCysProHis--- 931

Qy  2947 CAGAGCTTCCCCCCTGGCCCTCGGACCACAGCCTTCTGGACCTCCACCTCGACTCAGAGC-- 3004
Db   932 ---GlnArgProProCysIleSerProHisMetSerGlyProGlyLeuGlnAsnThr 951

Qy  3005 ------------------------CCCCTGCCTCAGGAGGAGACTTCGCTCTGGACCTCGA 3036
Db   952 rThrLeuAlaValHisCysProAlaSerValGlyThrValGluIleGlyAlaThrPr 971

Qy  3037 AGCACCCCTGCCT 3049
Db   971 oSerGluLeuArgSerSerMetValProProPheProSerGluProAlaProLeuGlyPr 991

Qy  3005 oSerProValPro 995
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OS   Drosophila melanogaster (fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=OREGON-R; TISSUE=HEAD;
RX   MEDLINE=94211879; PubMed=8159766;
RA   Warmke J.W., Ganetzky B.;
RT   "A family of potassium channel genes related to eag in Drosophila and
RT   mammals.";
RL   Proc. Natl. Acad. Sci. U.S.A. 91:3438-3442(1994).
RN   [2]
RP   SEQUENCE OF 1-102 FROM N.A.
RC   STRAIN=BERKELEY;
RA   Celniker S.E., Aghavani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA   Chew M., Doyle C.M., Farfan D.E., Flanagan J., Houston K.A.,
RA   Hunmasti S.R., Karra K., Kearney L., Kim S.H., Lee B., Lomotan M.A.,
RA   Mazda P., Mok M.S., Moshrefi A.R., Mok M.S., Moshrefi A.R., Nixon K.,
RA   Park S., Pfeiffer B., Punch D., Snir E., Twomey B., Wan K.H.,
RA   Whitelaw K.R., Yee A., Zhang R., Zieran L.L., Kimmel B.E.;
RL   Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 103-1284 FROM N.A.
RC   STRAIN=BERKELEY;
RA   Celniker S.E., George R.A., Galle R.F., Hoskins R.A., Svirskas R.R.,
RA   Harris N.L., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
RA   Chavez C., Chew M., Doyle C.M., Farfan D.E., Flanagan J.,
RA   Houston K.A., Hunmasti S.R., Karra K., Kearney L., Kim S.H., Lee B.,
RA   Lomotan M.A., Mak J., Mazda P., Mok M.S., Moshrefi A.R., Moshrefi M.,
RA   Nixon K., Pacleb J.M., Park S., Pfeiffer B., Punch E., Snir E.,
RA   Twomey B., Wan K.H., Whitelaw K.R., Yee A., Zhang R., Zieran L.L.,
RA   Kimmel B.E.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; U04246; AAA62472.1; -.
DR   EMBL; AC004640; -; NOT_ANNOTATED_CDS.
DR   EMBL; AC005298; -; NOT_ANNOTATED_CDS.
DR   FlyBase; FBgn0011589; elk.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; IPR000027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50042; cNMP_BINDING_3; 1.
KW   Ionic channel; Polymorphism.
FT   VARIANT   1127   1127   I -> L (IN STRAIN BERKELEY).
SQ   SEQUENCE   1284 AA;   141377 MW;   F09C418E19394A04 CRC64;

Alignment Scores:

Pred. No.:
Alignment No.:　　　1.14e-97
Score:　　　　　　　1901.00　　　Length:　　　　　1284
Percent Similarity:　53.85%　　　Matches:　　　　　455
Best Local Similarity:　40.77%　　　Conservative:　　146
Query Match:　　　　31.22%　　　Mismatches:　　　273
DB:　　　　　　　　5　　　　　　Indels:　　　　　242
　　　　　　　　　　　　　　　　Gaps:　　　　　　31

US-09-965-830-1_COPY_6_3257 (1-3252) x Q23974 (1-1284)

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Qy    1 ATGGCGGCCACGATGGCGGGGGCCTCCTGCGGCCTCAGAACACCTTCCTGGACACCATCGCGGTACG 60
        |||||||||    ::||||||||||||||||||  ::|||||||||||||||||||||||||||||
Db    1 MetProAlaArgLysGlyLeuLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 20

Qy   61 CGCTTCGACGGCACGGCACGCAGTAACTTCGTGTGGGCAACCGCCCAGTGTGGGGCTGCTTC 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |||
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(Sequence alignment continues in the right column)

Db   21 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn 39

Qy 121 CCCGTGGTGTTACGTCCTCGTGATGGCTTCTGTTCTGTTACTTAGGGCGGCTTCTCCCGGGTC 180
        ||| ::|||| |||||||||||||||||||||||||| :||||||||||||||||::::
Db   40 ProIleValThrCysSerSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle 59

Qy 181 ATGCAGCGCGGGGGCGTGTCGGCCTCCTTCCTTTATGGGCCAGACACCAGTGAGCTCGTCGGC 240
        ::||||||||||||||||||||||||||||||||||||||||||||| :::::::::::
Db   60 MetGlnArgGlyGlyValSerCysHisPheLeuTyrGlyProAspThrLysGlyLeuValGly 79

Qy 241 CAACAGATCCGGCAAGGCCCTGGACGAGCAGCACAGGGAGTTCAAGGCTGAGCTGTTCGTAC 300
        ::|||| |||||||||||| |||:|||| || :|||||||||||||||||||| ||:|||
Db   80 GlnGlnIleGlyLysSerLeuAspGluGlnHisArgGluPheLysAlaGluLeuPheVal 99

Qy 301 CGGAAGAGCCGGCGGCTTCCCGTTCGTTCTCGTGTCTTCTCCGGATGTGAATACCCCATAA 360
        ::||||||||||||||||||||||||||||||||||||||| :||::||||||||||||
Db 100 LysLysGluGluAlaProHeePCysLeuPheAsnProIleValProIleLysGluLys 119

Qy 361 GGGGAGGGTGGCCTCTTCCTAGTCTCTCACCAAGGACATCACGGAAAACCAAG------ 411
        ::::|||||||||||||||||||||||||||| ||||||||||||||||:::
Db 120 ArgAspValValLeuPheLeuValAlaSerHisLysAspIleThrHisThrLysMetLeuGlu 139

Qy 411 -- 411
Db 140 MetAsnValAsnGluGluCysAspSerValPheAlaLeuThrAlaAlaLeuLeuGlyAla 159

Qy 412 -- 412
Db 160 ArgPheArgAlaGlySerAsnAlaGlyMetLeuGlyLeuGlyLeuProGlyLeuGly 179

Qy 421 GGCCCC-----------GACAGATGGAGGAGAGACAGGTGGTGGCCGGCGGCCGATATGGGCGG 471
        ||||||| ||| ||||||||| :::::
Db 180 GlyProAlaAlaSerAspGlyAspThrGlyLeuGlyLeuGlyAsnAsnLeuAspValPro 199

Qy 472 GCACGAGATCCAAAGGCTTCAATGCCACCACCGGCGGAGCCCGGGCCGGCTGCTTACCACCTG 531
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 200 Ala----------GlyCysAsnMetGlyMetGlyMetGlyMetGlyMetGlyMetGluLeu 216

Qy 532 TCCGGGCACCTGCAGAAGCAGCCCAAGGGC---------AACCACAAGCTCAATAAGGGG----- 582
        ||||||||| ::: ||| ||||
Db 217 SerGlyHisTyrLysProGlyLysGlyValLysThrLysGlyLeuLysLeuGlyAsnAsn 236

Qy 583 ---GTGGTTTGGGGAGAAACCAAACTTGCCTGAGTACAAAGTAGCCGCCGCCATCCGGAAGTCG 639
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Db 237 PheMetHisSerThrGluAlaProPheProGluTyrLysThrGlnSerIleLysLysSer 256

Qy 640 CCCTTCAATCCTGTTGCACTGTGGGCGCCACTGGAGCGCACCGCCAGGTGGTGTGTT 699
        ||||||| ||| :::
Db 257 ArgLeuIleLeuProHisTyrGlyValPheGlyGlyIleThrPAspPrpValIleLeuVal 276

Qy 700 GCCCACACTCTATGTGTGGCTGTGCCACTGCCCTACCAGGGTGTGTGTGTTGTAGCACAGCACGGGAG 759
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Db 277 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaAlaPheAlaLysAlaAspArg 296

Qy 760 CCCAGTGCCGCGGGCGGCCGCGGCCCAGCGTCGTGACCTGGCGGTGGAGGTGCCTCTCATC 819
        ||| :::
Db 297 GlnThr----------LysValSerAspValIleValGluAlaGluLeuPheIle 310

Qy 820 CTTGACATTGTGTGCGAAATTTCCGTACCACATTCGTGTCCAAGTGGGGCCAGGTGGTGTT 879
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Db 311 ValAspPheIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyLeuLeuLeuVal 330

Qy 880 GCCCCAAAAGTCCATTTGCCTCACTACGGTCACACCACCTGGTTCCTGCGATGTCATCGCA 939
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Db 331 AsnSerLysGlnIleAlaIleLeuAsnTyrLeuArgGlyTrpPheLeuAlaLeuAspAspAla 350

Qy 940 GCGCTGCCCTTTGACCTGCTACATGCCTTCAAGTCAACGTGTACTTACGGG------------ 990
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Db 351 AlaLeuProPheAsp--------HisLeuTyrAlaSerAspLeuTyrAspGlyLeuAspSer 368

Qy 991 ---GCCCATCTGCTGAAGACAGGTGGCCTGCGCGGCCTGCTGGCGGTGCGTGCTGCTCATCGCTG 1047
        :::||||||| || ||::::
Db 369 HisIleHisLeuValLysLeuThrArgLeuLeuAlaLeuArgLeuLeuGlnLysIle 388
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Qy   1048 GACCGGTACTCGCAGTACACGGCCGCGTGGTGCTGCTCATGGCCGTGTTCGCCCTG 1107
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Db    389 AspArgTyrSerGlnHisThrAlaAlaMetIleLeuThrLeuLeuMetPheSerThrLeu 408

Qy   1108 CTCGGCCACTGGCTGCTGCTGCTCTGGTTTTACATTGGGATCGAGACGAGC      1167
          ||||||||:::|||::||||||||:::|||:::||||||||||
Db    409 AlaAlaHisTrpLeuAlaCysIleLeuThrTyrValIleAlaValLysGluTyrGlu     426

Qy   1168 GAATCGGAGCTGCCTCAG------AATTGGGCTGGGCTGCCAGGACTGGGCCGGCGACTGGGAG 1221
                               |||||||
Db    427 -----TrpPheProGluSerAsnIleGlyTyrrpLeuGlnLeuLeuValAlaGluArg----- 442

Qy   1222 ACTCCCTACTACCTGGTGGGCGGCGGGAGGCCAGCTGGAGGCAACAGCTTCGGCCAGAGTGAC 1281
          ||||||
Db    442 ----------------------------------------------------------- 442

Qy   1282 AACTGCAGCAGCAGCGCAGCCCCACGCGGGGCTGCTGGGACTGGGGGCCCGTCG        1341
             |||
Db    443 -----LysAsnAlaSerValAlaIleAlaIleLeuThrThrAlaGlu----------    454

Qy   1342 CTGGCGAGCGCCTACATCACCCTCTACTTCGCACTCACTCGGACCGGTGGC          1401
          |||
Db    455 -----ThrTyrSerThrAlaLeuTyrPheThrPheThrSerLeuThrSerValGly    471

Qy   1402 TTCGGCAACGTGTCCGGCCAACACGGACACCGGAGACGTC...                 1461
          |||||||
Db    472 PheGlyAsnValSerAlaAsnThrThrAlaGluLysVal...                 491

Qy   1462 ATCGGGCGCCTGATGCACGCGGTGGTGTTGGGAAGCTGACGCGCCATCATCAGCGCATG 1521
          |||
Db    492 IleGlyAlaLeuMetHisAlaValValPheGlyAsnValThrAlaIleIleGlnArgMet 511

Qy   1522 TACGCCCGCGGCGTTTCTGTACCACACACGCCGCACGGGTCCGACTACATCCGCATC   1581
          |||
Db    512 TyrSerArgArgSerLeuTyrGluSerLysTrpArgAspPheLeuLysSerPhe...   531

Qy   1582 CACCGGTATCCCCAAGCCCCTCGAGTACTTCCAGGCCACCACCTGGCCG           1641
          |||||||
Db    532 HisAsnMetProLysGluLeuLysGlnAlaThrTyrPheGlnThrSerTrpSer     551

Qy   1642 GTGAACAATGGCACTCGACACCACCGAGTGCTGCTGGAGAGCCTGCGCGCGCA      1701
          |||
Db    552 LeuSerHisSerGlyIleLeuTyrGluThrLeuArgGluPheProGluLeuArgGly 571

Qy   1702 GACATCGCCCATGCACCTGCACCTGCACCAAGGAGTCCTCGCCACTGTTGAGGCGGCCAGC 1761
          |||
Db    572 AspValSerMetHisLeuHisArgGluIleLeuLeuProIlePheGluAlaAlaSer   591

Qy   1762 CGCGCGCTGCCTGCGGCGGCCACTGTCTCTGGGCCCCCGCCTTCGCACCGGGGGGAG  1821
          |||||||
Db    592 GlnGlyValCysLeuGluLysSerLeuLeuSerLeuuHisIleLeuLysThrAsnPheCys 611

Qy   1822 TACCTCACTCCACCCAAGGCCCATGCCGTCGCAGGCCGGCCTCTACTTTTGTCTGCTCTCTGGCCTCCATG 1881
          ||||||
Db    612 TyrLeuLeuHisLysGlyAspAlaLeuAsnTyrIleTyrrLeuCysAsnGlySerMet   631

Qy   1882 GAGGTGGCTCAAGGGTGGCCACCGTGCTGCGCCATCCTAGGGAAGGCGGCGACCTGATCGGTGT 1941
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Db    632 GluValIleIleLeuLysAspAspMetValValAlaIleLeuGluGlyLysGlyAlaGlySer 651

Qy   1942 GAGCTG------                                                    1947
          ||||||
Db    652 AspIleLeuAsnValHisLeuThrSerAsnGlyGlnMetThrAlaThrThrAsnSer    671

Qy   1948 CCCGGGCGGAGCAGGTGGTAAAGGCCAATGCCGACGTGAAGGGGCTGACGTACTGCGTC      2007
          |||:::||||||
Db    672 AlaGlyGlnAsnProValValAlaArgSerSerAspIleLeuThrThrTyrCysAsp   691

Qy   2008 CTGCCAGTGTCTGCACGACCTTGCGCGTGTACCCCGGAGTTGCC                   2067
          |||||:::|||:::|||
Db    692 LeuLysCysIleHisMetGlyLeuValGlyLeuuValLeuArgLeuTyrProGluTyrGln  711
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Qy   2068 CCGGCGCTTCAGTCGTCGGTGCCCTCCGAGGGGGAGCTCAGCTACACAAACCTGGGGTCTGGGGAGGC 2127
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Db    712 GlnGlnPheAlaLeuAsnAspIleGlnHisAspLeuuThrCysAsnLeuArgGluTyrGlu 731

Qy   2128 TCTGCAGAGGTGGACACAGC                                        2169
          :::|||
Db    732 AsnGlnAsnAspSerAspIleGlyLyProSerPheProSerIleSerGluAspAspGlu 751

Qy   2170 CTTATGTCCACGCTGGAG------                                    2214
          |||
Db    752 AsnArgGluGluAlaGluGluGlyLyGlyLysGlyGlyLyGlyGly----Gly 769

Qy   2215 CCC-                                                       2250
          |||
Db    770 ProProSerGlyAlaSerProLeuHisSerAsnIleSerAsnSerProLeuHisAlaThrArg 789

Qy   2251 AGCCCCCTGCTGTCCCCTGGCTGACCCTCCATCCTCAGCTGCCAAGCTGCTATCCCCA 2310
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Db    790 SerProLeuLeuGlyMetGly----------------------------SerPro 798

Qy   2311 CGTCGGAACAGCACCCCGGCCCTCGTCTTAGGTGGCAGAGGGGAGGGCAGGCGGGGCT 2370
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Db    799 Arg--------------AsnGlnArgLeuHisGlnArgGly----------- 807

Qy   2371 TTGAAGGCTGAGGGTGGCCCTCTGCTCCCCACGGGCCCTTAGAGGGGCTACGGCTGCC 2430
          |||||
Db    808 ---GluGluProGlyProLeuGluGlu                                814

Qy   2431 CCCATGCCATGGAAATGTGCCCCCAGATCGAGCCCCAGGGTAGTGGCATTGNAGAC     2490
          |||
Db    815 ------------GluThrAsnLysArgHisArgThrLeuAsnAla----------- 825

Qy   2491 GGCTGTGGGTCGGGACCCAGCCCCCAAAGTTCTCTTTCCCGCGGTGGGCTGTGGCCCGGGAATGT 2550
          |||:::
Db    826 AlaCysSerProLeuAspArgGlySerPhe                            834

Qy   2551 AGCAGCAGCCGCCCTCCCCTGGACCAGAGAGCGGGGCCTGCTCACTGTTCCCANGGGCCCAGC 2610
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Db    835 ---GluGluProGluLeuGluGlu---------------------------GlnSer 845

Qy   2611 GAGGCAAGGAACACAGACACTGGACAAGCTTGCGGCAGGCGGGTGACAGAGCTGTGCAGAG 2670
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Db    846 SerGlyGlyLysProSerLeuGluArgLeuGlnValSerThrAlaSerGln 865

Qy   2671 CAGGTGCTGCAGATGCGGGAGAGCTGCAGTGCACTGGGGCATCCTGCTCCACCTTGTCCTG 2730
          |||:::
Db    866 AspValAlaLeuGlnLeuuSerArgAlaGlyAsnAlaIleSerAlaLeuGlnGluMet--- 884

Qy   2731 GCGCCCCACAGGGAGAGGGGTCCGTGCCCTCCGGGGCCATCGGGGAGGAGGGCGCCCAGAGC 2790
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Db    885 -----------------------------------------------------ThrPhe 886

Qy   2791 ACCTCCGGGCTTCTGCAGCCTCGTGTGTGGACACTGGGGCATCCTCCTACTGGCCTTCCTG 2850
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Db    887 ThrSerSerAsnAlaMet----------------ThrSerHisSerLeuLysPhe--- 899

Qy   2851 CCCCAGCTGGCCTCGTC-----TTGAGTGGGGACTTGGCCCCCACCCTCGTCCGGGGGCCT 2904
          |||||
Db    900 ProProAlaArgSerIleProAsnIleSerGly---ValAlaGlyThrArgSerGlyValA 919

Qy   2905 CCTCCCCTCATTGGCACCCCTGGGCGTGGTCCCCACCGGTCTCAGAGCCTCCCCTGGCCT 2964
          :::|||
Db    920 lavalGluHisGlyLeuMetGly---GlyValLeuAlaiAlaGluLeu--AlaAlaMe 937

Qy   2965 CGAGCCACAGCGTTTCTGGACCTCCACCT-----------CAGACTCAGAGCGCCCCTGCC 3012
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Db    937 tGlnArgSerSerHisSerProProGluuValTrpGlyArgAspValGlnLeuProThrSe 957

Qy   3013 TCAGGAGGACCTGTGCTGGAGCCCAGCACCCCCTGCCTCCC                   3052
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ID   Q9V899      PRELIMINARY;      PRT;   1311 AA.
AC   Q9V899;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ELK protein.
GN   ELK OR CG5076.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nixon K.A., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Zheng L.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
DR   EMBL; AE003801; AAF57772.1; -.
DR   FlyBase; FBgn0001589; elk.
DR   InterPro; IPR000555; cNMP_binding.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM00086; PAC; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS50042; CNMP_BINDING_3; 1.
SQ   SEQUENCE   1311 AA;  144467 MW;  A766C460B833329B CRC64;
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US-09-965-830-1_copy_6_3257 (1-3252) x Q9V899 (1-1311)

DB:
Alignment Scores:
Pred. No.:              1.15e-97       Length:          1311
Score:                  1901.00        Matches:         455
Percent Similarity:     53.85%         Conservative:    146
Best Local Similarity:  40.77%         Mismatches:      273
Query Match:            31.22%         Indels:          242
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Qy    1 ATGGCGGCCATGCGGGGGCGGGCCCTTCCTCGGCGCCGTCAGAACACCTTCCTGGACACCATGCTACG 60
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Db   28 MetProAlaArgLysGlyGlyLeuLeuAlaProGlnAsnThrPheLeuAspThrIleAlaThr 47

Qy   61 CGCTTCGACGGACGCACAGTAACTTCTTCGTGCTGGGCACGCGCCCAGGTGGCGGGGCTCTTC 120
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Db   48 ArgPheAspGlyThrHisSerAsnPheValLeuGlyAsnAlaGlnAlaAsnGly---Asn 66

Qy  121 CCCGTGGGTCTACTTGCCTCGATGGGCTTCTGTGACCTCACGGGGCTTCCGGGGTGAGGTC 180
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Db   67 ProIleValTyrCysSerAspGlyPheValAspLeuThrGlyTyrSerArgAlaGlnIle 86

Qy  181 ATGCAGCGGGGGGCTGTGCCCGCCTCCTTCCTTTATGGGCCAGACACCACCAGTGAGTCGTCCGC 240
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Db   87 MetGlnLysGlyGlyCysSerCysHisPheLeuTyrGlyProAspThrLysSerLys 106

Qy  241 CAACAGATCCGCAAGGGCCCTGGACGAGCACACAAGGAGTTCAAGGCTGAGCGGATCCTCTAC 300
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Db  107 GlnGlnIleGluGlySerLeuSerAspHisLysAspSerLeuThrHisThrLysMetLeuGlu 126

Qy  301 CGGAAGAGCGGGGGCTCCCGTTCGTGTTCTCGGTGTTCGTCTGGATGTGATACCCATAAAGAATGAGAAA 360
          |||||||||       :::|||||||||||||
Db  127 LysLysGlyGluGlyAlaProAlaProPheCysSerLeuPheAspLysGluValProIleLysAsnGluLys 146

Qy  361 GGGGAGGTGGGCTCTCTTCCTAGTCTCTCACAAGGACATCAGCGAAACCAAG--------- 411
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Db  147 ArgAspValPheLeuAlaSerHisLysAspSerLeuThrHisThrLysMetLeuGlu 166

Qy  412 ------------------------------------------------AACCGAGGG 420
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Qy  411 ------------------------------------------------- 411
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Qy  421 GGCCCC------------GACGAGGAAGGAAGACAGGTGGGTGGGCCGGCCGGCGGGAGTCG 471
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Db  207 GlyProAlaAlaSerAspGlyAspThrGluLeuGlyGluGlyAsnAsnLeuAspValPro 226

Qy  472 GCACGATCCAAAGGCTTCAAATCCCAACCACGGGCCGGGAGCCGGGCCGGTGCTCTCTACCACTG 531
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Db  227 Ala-----GlyCysAsnMetGlyArgArgSerArgAlaValAlaLeuTyrGlnLeu 243

Qy  532 TCCGGGCCACCTGCCAGAAGCAGCGCCCAAGGGC---AAGCACAAGGCTCAATAAGGGG----- 582
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Db  244 SerGlyHisTyrLysProGluLysGlyValGlyValLysThrLysGlyLeuGlyAsnAsn 263

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Db  264 PheMetHisSerThrGluIleAlaProPheProGluThrTyrTyrLysThrGlnSerIleLysLysLysSer 283

Qy  640 CCCTTCATCCTGTTGCACTGTGGGGACTGAGAGCGCACCTGGGAGGATGGCTTCATCCTGCTC 699
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Qy  700 GCCACACTCTATGTGGCTGTCACTGTGCCCTACAGCGGTGTGTTGTGACCACCACGGGAG 759
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Db  304 AlaThrPheTyrValAlaLeuMetValProTyrAsnAlaAlaPheAlaLysAlaAspArg 323

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Qy    820 CTTGACATTGTGTCGAAATTCCGTACCACATTGTGTCCAAGTCGGGCCCAGTGGTGTTT 879
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Db    338 ValAspIleLeuLeuAsnPheArgThrThrPheValSerArgLysGlyLeuValSer 357

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          |||  |||||||||::::|:||||    ||||||||||:::||||
Db    358 AsnSerLysGlnIleAlaIleAsnTyrLeuArgGlyTyrProAlaLeuGluAspLeuLeuAla 377

Qy    940 GCGGCTGCCCTTTGACCATGCTCATGCCTTCAAGGTCAACGTGTACTTCGGG------ 990
          |||||||||||||||||||||||||||||::: |||
Db    378 AlaLeuProPheAsp------HisLeuTyrAlaSerAspLeuTyrArgAspGlyGluAspSer 395

Qy    991 ---GCCCATCTGCTGAAGACGGGTGGCGCGGTCCCTTCCGGGGCTG 1047
             :::||||||||||||||||||||||||||||||||||||
Db    396 HisIleHisLeuValLysLeuThrArgLeuLeuLeuGlnLysIle 415

Qy   1048 GACCGGTACTCCGAGTACGACAGCCCGCGCCCGTTGCTGCTGGTCCGGTTTCATCCCCTG 1107
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Db    416 AspArgTyrSerGlnHisThrAlaMetIleLeuThrLeuLeuSerPheThrLeu 435

Qy   1108 CTCGGCACTGGGGTCGGGCTGTCGGTTTTACATTGGCCACGGGGAGATCGAGAGCAGC 1167
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Qy   1168 GAATCCAGCTCGCCTGAG------ATTGGCTGGCCGTGGCCCGGCGCGTGGGCCCCTG 1221
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Db    454 ------TrpPheProGluSerAsnIleGlyTyrTrpLeuGlnLeuLeuAlaGlyArg------ 469

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Db    469 469

Qy   1282 AACTGCACGAGCAGCAGGGAGGGCCAACCGGGACGGGTGCTGGGGGTGCCCGTCG 1341
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Db    470 ------LysAsnAlaSerValAlaIleLeuThrThrAlaGlu-- 481

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Db    482 ------ThrTyrSerThrAlaLeuGlyTyrPheThrPheThrSerLeuThrSerValGly 498

Qy   1402 TTCGGCAAGCTGTCGCCGACACGGACACCGAGAAGATCTTCTCCATCTGCACCATGGCTC 1461
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Db    499 PheGlyAsnValSerAlaAsnThrThrAlaGlyLysValPheThrIleIleMetMetLeu 518

Qy   1462 ATCGGGGCGCCCTGAGTGCACGCGGTGGTGTTGTTGGGAAACGTGACGGCCCATCACCACGGCATG 1521
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Db    519 IleGlyTyrAlaLeuMetHisAlaValAlaValPheGlyLysAsnValThrAlaIleIleGlnArgMet 538

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Qy   1762 CGGGGCTGCCGGGGCACTGTCTCTGGCCCTTCGACAGCCCGGGGGAG 1821
          :::||||||||||||||||||||||||||
Db    619 GlnGlyCysLeuLysLeuGlnHisLeuSerLeuHisIleLeuTyrThrAsnPheCysAlaProGlyGlu 638

Qy   1822 TACTTCCATCCACCAAGGGCCGATGCCCTGCAGGCCCCTTCACTATTGTGTCCTCTGGCTCCATG 1881
          ::||||||||||||||||||||||:::|:||||
Db    639 TyrLeuLeuHisLysLysGlyAspAlaLeuAsnThrIleLeuTyrTyrCysAsnGlySerMet 658
```

```
Qy   1882 GAGGTGCTCAAGGGTGGCACCGTGCCTGCCGCCATCCTAGGGAAGGGCGACCTGAT 1941
          :::||||||||||  |||
Db    659 GluValIleLysAspMetValAlaIleLeuLeuGlyLysGlyAspLeuValGlySer 678

Qy   1942 GAGGTG------ 1947
          |||||||
Db    679 AspIleAsnValHisIleLeuValAlaIleThrSerAsnGlyGlnMetThrAlaThrThrAsnSer 698

Qy   1948 CCCGGCCGGGACAGGTGGTTAAAGGCCAATGGCCAGTGAACTGAAGGGCGTGACGTACTGGGTC 2007
          ::::: |||||||||||||||||||:::
Db    699 AlaGlyGlnAsnValValArgSerSerAspIleLysAlaLeuThrTyrCysAsp 718

Qy   2008 CTGCAGTGTCTGCACGTGGCCTGGCCGCACGACACCACCTTCGCGTTACCCGAGTTTGCC 2067
          |||::::|||||||||||||||||||||||::::
Db    719 LeuLysCysIleHisMetGlyGlyLeuValValLeuGluLeuArgLeuTyrProGluTyrGln 738

Qy   2068 CCGGGCCTTCAGTCGTGGCCTCCGAGGGGAGCTCAGCTACACAAGCCTGGGTGCTGGGGAGGC 2127
          |||||||||||||||||||||||||||||::::
Db    739 GlnGlnPheAlaLAsnAspIleGlnHisHisAspPheLeuThrHisTyrGluTyrGlu 758

Qy   2128 TCTGCAGTGTCTGCACGTGGACCACAGC- 2169
          |||
Db    759 AsnArgGlyLysIleGlyLysGlyLysGlyLysGlyGly------ 778

Qy   2170 CTTTATGTCCACGCTGGAG------ 2214
          |||||||||||||||
Db    779 AsnArgGluGluValAlaGluValGluValLysGlyLysGlyLysGlyGly------Gly 796

Qy   2215 CCC------ 2250
          :::
Db    797 ProProSerGlyValAlaSerProLeuHisAsnIleSerAsnSerProLeuHisAlaThrArg 816

Qy   2251 AGCCCCCTGCTGTCCCCTGGCTGCCACCTCCATCCTGCCAAGCCTCTATCCCA 2310
          |||||||||||||||||||:::
Db    817 SerProLeuLeuGlyMetGly------ 825

Qy   2311 CGTCGAACACGACCCCGGGCTCGTCTTAGGTGGCGCAGAGGGGCCAGGCAGGGGCT 2370
          |||||||||||||||||||||::::
Db    826 Arg------AsnGlnArgLeuHisGlnArgGly 834

Qy   2371 TTGAAGGCTGAGGCTGGCCCCCTCGCTCCCCACGGGCCCTTAGAGGGGCTGCCC 2430
          |||||||||||||||||||||||||:::
Db    835 ------ArgSerLeuIleThrLeuArg 841

Qy   2431 CCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCCAGGGTAGTCAGGTTAGGATGGCATTGAAGAC 2490
          |||||||||||||||||||
Db    842 ------GluThrAsnLysArgHisArgThrLeuAsnAla------ 852

Qy   2491 GGCTGTGGGCTGGGACCAGCCCAAAGTTCTCTTTCCGCGGTGGGCCCAGTGTGGCCCGGAATGT 2550
          ||||::::|||
Db    853 AlaCysSerLeuAspsPARGGlyGlySerPhe------ 861

Qy   2551 AGCAGCAGCCCCTCCCCTGGACAGAGACGGCGGCCTGCTCACTGTTCCCCATGGGCCCAGC 2610
          |||||||||||||||||||||||:::
Db    862 ---GluGluProGluProLeuGluGlu------ 872

Qy   2611 GAGGGCAAGGAACACAGAACACTGGACAAGCTTCGGGACGCCGGTGACAGAGCTGTCAGAG 2670
          |||::::|||||||||
Db    873 SerGlyGlyLysGlyArgProSerLeuGluArgLeuAspSerGlnValSerThrLeuHisGln 892

Qy   2671 CAGGTGCTGCAGATGCGGGAAGGACTGCCAGTCGACTTCGGCCAGCCGGTTGTCCTG 2730
          |||||||||||||||||||||||||||||:::
Db    893 AspValAlaGlnLeuSerAlaGluValArgasnAlaIleSerAlaLeuGlnGluMet--- 911

Qy   2731 GCGCCCCCACAGGGAGGAGGTGTCCGTGCCCTCCGGGGCCGGGAGGGGCGCCCAGCAG 2790
          ||||||||||||||||||||||
Db    912 ------ThrPhe 913

Qy   2791 ACCTCCGGGCTTCTGCAGCCCTCTGTGTGTGGACACTGGGGGCANCCTCCTACTPGCCCTGC 2850
          ||||||:::
Db    914 ThrSerAsnAlaMet------ 926

Qy   2851 CCCCCAGCTGGCTCTGTC------TTGAGTGGGACTTGGCCCCACCTCGTCGGGGGCT 2904
```

```
Db    927 ProProAlaArgSerIleProAsnIleSerGly--ValAlaGlyThrArgSerGlyValA 946
          ||||||      :::||||::       ||||||
Qy   2905 CCTCCCCATGGGACCCGGGGCCCTGGGCGCCGGTCCCCAGCGTTCCCTTCCTTTAT 2964
          ::      ||||||    :::          ||||||
Db    946 IaValGlyHisGlyLeuMetGly---GlyValLeuAlaAlaLeuGlyLeu--AlaAlaMe 964
          ||||||
Qy   2965 CGACCCACAGCTTTCTGGACCTCCACCT---------CAGACTCAGAGCCCCTGCC 3012
          :::      ||||||      |||
Db    964 tGlnArgSerSerHisProProGluValTrpGlyArgAspValGlnLeuProThrSe 984
          |||::::                      |||::::::
Qy   3013 TCAGGAGACCTCTGCTCTGAGCCCAGCACCCCTGCCTCCC 3052
          |||::::      |||::::::      |||
Db    984 rAsnThrAlaSerSerLysAlaProSerProValGluPro 997
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RESULT 11
Q9TSZ3

Alignment Scores:
Pred. No.:
Score: 3.14e-78
                            1551.00   Length: 1158
Percent Similarity: 44.40%   Matches: 411
Best Local Similarity: 33.36%   Conservative: 136
Query Match: 25.47%   Mismatches: 351
DB: 6   Indels: 334
                                               Gaps: 33

US-09-965-830-1_copy_6_3257 (1-3252) x Q9TSZ3 (1-1158)

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Qy    1 ATGCCGGCCATCGGGCGCCGGGGCCTCAGCAAAACACCTTCTGGACCACCGCTACG 60
        ||||||      ||||||      :::||||||
Db    1 MetProValArgGlyHisValAlaProGlnAsnThrProPheLeuAspThrIleIleArg 20

Qy   61 CGCTTCGACGGGACGACACAGTAACTTCGTCGCTGGGCAACGCGCCAGGTGCGGGGGTCCTCTTC 120
        :::||||||:::||||::      ||||||:::||||||
Db   21 LysPheGluGlyValGlnSerArgLysPheIleLeuAlaAsnAlaArgValGluAsnCys-- 39

Qy  121 CCGGTGGTACTGCTCTGATGAGGCTTCACGGGCTTCTCCGGGGCTGAGGTC 180
        ||::||||||      ||||::::||||||      |||||||||||::::||||||
```

```
Db   40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59
        |||||||||||      :::||||
Qy  181 ATGCCAGGCGGGCGTGCGCTGCTGCCTGCGCGTCGTCCTTCCTTTATGGGCCGCAACAGC 240
        |||||||      ||||||:::||||||
Db   60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgAlaAla 79
        |||||||:::||||||
Qy  241 CAACAGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGGCTGACCTGTAC 300
        ||||||      :::||||||      |||
Db   80 AlaGlnIleAlaGlnIleAlaLeuLeuGlyAlaGluGlnArgLysSerGluIleAlaPheTyr 99
        |||:::||||||      |||::::::
Qy  301 CGGAAGAGGCGGGCGCTCCGGTTCTCGTGGTGCTCCCGGATGAATCCCATAAAGAATGAGAA 360
        ||||||      |||::::||||||      |||::::::
Db  100 ArgLysAspGlySerCysPheLeuCysLeuValAspSpValProValLysAsnGluAsp 119

Qy  361 GGGGGAGGTGGGCTTCTCTTCCTA----------------GTCTCACAAGGACATC 399
        ||||||:::||||||      |||::::::      |||
Db  120 GlyAlaValAlaIleIleMetPheIleLeuAsnPheGluLeuLysSerAspMetValGly 139

Qy  400 ----------AGCGAAAACCAAGAACCGAGGGGGCCCCACAGAGGAAGGAGGACAGGT--- 447
          :::||||      ||||||:::||||||
Db  140 SerProThrHisAspThrAsnHisArgGlyProProThrSerTrpLeuAlaProGlyTyrArg 159

Qy  447 ------------------------------------------------------------ 447
Db  160 AlaLysThrProPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrThrArgGluSerSer 179

Qy  447 ------------------------------------------------------------ 447
Db  180 AlaAlaArgProGlyGlyValGlySerAlaGlyAlaProGlyAlaValValAspValAsp 199

Qy  447 ------------------------------------------------------------ 447
Db  200 LeuSerProAlaValProSerArgGluSerLeuAlaLeuAspGluValThrThrAlaMetAsp 219

Qy  447 ------------------------------------------------------------ 447
Db  220 AsnHisValAlaGlyLeuGlyProMetGluGlnAlaLeuLeuValGlySerSer 239

Qy  447 ------------------------------------------------------------ 447
Db  240 ProProAlaGlyValAlaProGluProLeuProSerProArgAlaHisSerLeuAsnProAsp 259

Qy  448 -----GGTGGCCGGGCGCCGATATGGCCGGGGCGGACGAGTCCAAAGGCTTCAATCCCACCGG 501
        ||||||||||:::::||||||
Db  260 AlaSerGlySerSerCysSerLeuAlaArgThrArgSerGluSerCysAlaSerVal 279

Qy  502 CGGCGG-------------------------------------------------- 507
        ||||||
Db  280 ArgArgAlaSerSerAlaAspAspAspIleGluAlaMetArgAlaGlyLeuProProPro 299

Qy  508 -----AGCCGGGGCGCGTGCTCTACCACCTGTCCGGGACCACCTGCAGAAGCAG----- 552
        |||      :::::      |||      |||
Db  300 ArgHisAlaSerThrGlyAlaMetHisProLeuArgGlyLeuLeuAsnSerThrSer 319

Qy  552 ------------------------------------------------------------ 552
Db  320 AspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThrLeuAsnPhe 339

Qy  552 ------------------------------------------------------------ 552
Db  340 ValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGluIleIleAla 359

Qy  553 CCCAAGGGCAAGCACAAGCTCAATAAGGGGGTGTTTGGGGAGAAACCAAC-------- 603
        ||||||      |||      :::      :::
Db  360 ProLysGlyLysHisLysLeuAsn------ValThrGluLysGlyValThrGlnValLeu 377

Qy  604 ----------TTGCCTGAGTACAAGAAGTAGCCGCCCATCCGGAAGTCCCCTTC 645
          |||||||||||      :::
Db  378 SerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnAlaProArgIleHisArgTrp 397

Qy  646 ATCCTGTTGCACTGTGGGGGACTGAGAGCCACCTGGGATGGCTTTTCCTTTACCCTGTCCCCACA 705
        :::||||||:::||||||      ||||||
Db  398 ThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuLeuVal 417
```

```
Qy    706 CTCTATGTGGCTGTGCTGCACTGTGCCTACAGCGTGTGTG--------AGCAGCACGG  756
          |||                                                    |||
Db    418 IleTyrThrAlaValPheThrProThrSerAlaAlaPheLeuLeuLysGluThrGluU  437

Qy    757 GAGCCCAGTGCC----------------GCCCGGCGGCCCAGCGTCGTGACCAGTGGCC  801
          |||                         |||
Db    438 GlyProProAlaProAspCysGlyThrArgLysGlnProLeuAlaValValAspPheIle  457

Qy    802 GTGGAGGGTCCTCTTCATCCTTGGACATTGTGCTACCACATTGTGGTCCCAAG  861
          |||||  |:::||||||||||:||||||||||||||||:::::||||||||
Db    478 AsnGluGlnValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrpPhe  497

Qy    862 TCGGGCCCAGGTGGTGGTTGTTGCCCCAAAGTCCATTTGGCCCCTACGTCACCACCTGGTTC  921
          ||||||||||||||||||||:::||||||||||:||:::||||||||||||
Db    498 LeuIleAspMetValAlaAlaIleProPheAspLeuLeu  510

Qy    922 CTGCTGGATGTCATCGGACAGGCCTGCCCTTTGACCTGCTACATGTGCTACTACGTG  981
          ||||| |||||||||||||::||||||||||||||||||||||:::|||||||||
Db    511 IleProGlySerGlySerGluGlyLeuLeuThrAlaArgLeuLeuArg  530

Qy   1024 CTGCTGGCCGGCTGCTTCCCGGCCTGGACCGGTACTGACAGGCCGTGGGGCTGGACA  1083
          |||||||||||||||||||||||||||:::||||||:::||||:||||||||||||
Db    531 LeuValArgValAlaAlaArgLysLeuAsnAlaArgTyrSerGlyTyrGlyValAlaAlaLeuPhe  550

Qy   1084 CTGCTCAATGGCCGTGTTCGCCCTCGCTCCGCGCCACTGGGTGGTTTTACATT  1143
          |||||||||||||||||||| ::||||||||||:|||||||||:::|||||||
Db    551 LeuLeuMetCysThrPheAlaLeuIleLeuAlaHisTrpLeuAlaCysSerIleTrpTyrAlaIle  570

Qy   1144 GGCCAGCGGGGAGAGAGCAGGAGGCAGGGAATCGAGATTGGCCTGAGAGTTG  1203
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db    571 GlyAsnMetGluGlnProHisMetAspSer--------ArgIleGlyTrpLeuHisAsn  587

Qy   1204 CTGGCCCCGACTGGAGACTCCCTACTTACCTGCTGTGGGCCCGGGAGGGAAC  1263
          ||||||||||||||||||:::|||||||||||||||||||||||||||||||
Db    588 LeuGlyAspGlnIleGlyLysProTyr  597

Qy   1264 AGCTCCGGGGCCAGAGCTGTGACAACTGCCAGCAGCAGCAGGCCAACGGGGCTGGAG  1323
          |||
Db    598 SerSerGly-  600

Qy   1384 AGCCTCACCAGGCGTGGGGCTTCGGCAACGTGTCCGCCAACACGGACAGAAGATCTTC  1443
          |||||| ||||||:::|||||||||||||||||||||||||||||||||||||||
Db    620 SerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIlePhe  639

Qy   1444 TCCAATCTGACCAATGCTCATCGGCCGCGGCCGCCGGTGGTTGTTTGGGAACCTGACG  1503
          ||||||||||||||||:||:::||||||||||||||||||||||||||||||
Db    640 SerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnValSer  659

Qy   1504 GCCATCATCCAGAGGCACATGTACGCGCCGCGCCTTTCTGTACCACACGCCGACCTG  1563
          |||||||||||||:::||||||||||||||||||:::|||||||||||||||||
Db    660 AlaIleIleGlnArgLeuTyrSerGlyTyrHisThrGlnMetLeuArgVal  679

Qy   1564 CGGGACTACATCGGCCATCGGAGCATGCTGGAGTAC  1623
          |||||| |||||:::|||||||||||||||||||
Db    680 ArgGluPheIleArgPheHisGlnIleProAsnProLeuArgLeuGluGluTyr  699

Qy   1624 TTCCAGGCCACCTGGGACGTGAACAATGGCATCGACACCACCGAGCTGCTGCAGAGCCTC  1683
          |||||||||||||||||||||||:::|||||||||||||||||||||||||||
Db    700 PheGlnHisAlaThrTrpSerThrTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGlyPhe  719

Qy   1684 CCTGACGAGCTGCGCGCAGACAATCGCCATCCACCTGCACAAGAGGTCCTGCAG---CTG  1740
          ||||||||||||| :::||||||||::: |||   |||||||||||||||||   |||
Db    720 ProGluCysLeuGlnAlaAspIleCysLeuHisLeuAsnArgSerLeuLeuGlnHisCys  739
```

```
Qy   1741 CCACTGTTTGAGGCGGGCCAGCGCGGCGGCGGCCGCGGTGCTGCGGGCACTGTCTCTGCGGGCGCCC  1800
          |||
Db    740 LysProPheArgGlyAlaThrLysGlyCysLeuArgGluAlaLeuAlaMetLysPheThr  759

Qy   1801 GCCTTCTGCACGCCGGGGGCGGGGCGGGAGTACCTCATCCACCAAGGCAATGCCTGCCGCCC  1860
          |||:||||| ||||||||||||||:::|||||||:||||:|||||||||||||||
Db    760 ThrHisAlaProProGlyAspThrLeuValHisSerAlaLeuAspLeuGluThrAlaLeuTyr  779

Qy   1861 TTTGTGTCTGCTCGTCCCCATGGAGGCTCAAGGGTGGCCACGGTGCCGCCCATCCTAGG  1920
          |||:|                            :::|||||||||||||||||
Db    780 PheIleSerArgGlySerIleGluIleLeuLeuArgGlyAspValValAlaIleLeuGly  799

Qy   1921 AAGGGGCCACCTGATCGGCTGGTGAGCCTGTGAGCTGCCCGGGGAGCAGGTGGTGAAGGCCAATGCC  1980
          |||
Db    800 LysAsnAspIleProPheGlyLeuProLeuAsnLeuThrTyrAlaArgProGlyLysSerAsnGly  819

Qy   1981 GACGTGAAGGGGCTGACGTACTGCGTCTGCCGGTCCTGCAGTGTCTGCAGGGGGGACGGGAGGACAGAGCTGGCCTGGGAC  2040
          ||||||||||||||:::||||||||||||||||||||||||:::|||||||||||||||||
Db    820 AspValArgGlyLeuThrTyrCysValCysArgSerCysSerValCysArgGlyAspGlyArgThrGluLeuAlaTrpAsp  839

Qy   2041 AGCCTTGCGCTGTACCCCGAGTTTGCCCGCGGCTTCAGTCTGTGGCCCCGAGGGAGCTC  2100
          |||
Db    840 ValLeuAlaAspMetTyrProGluPheSerAspHisTrpSerSerLeu--------GluIle  857

Qy   2143 ACCAGCTCCCGTGAGCGGCGACAATACCCTTATGTCCACGCTGGAGGAGGACAGAGAT  2202
          |||||||| :::||||||||||||||||||||||||:::|||||||||||||||||
Db    858 ThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGluLeuGlu  877

Qy   2203 GGGGAGCAGAGGCCCCACGGGTCTCCCAGCCACGTGATGAGCCCTCCAGCCCCTGCTG  2262
          |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    878 GlyGlyPheAsnArgGlnAsnArgLysLeuSerPheArgGlyArgArgProAspAsp  897

Qy   2323 CCCCGGCCTCGTCTCTAGGTGGCAGAGGGGGAGAGGCCAGGGGAGGGGTTTGAAGGCTGAG  2382
          ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    914 AlaGlyPro--------SerGlyArgGlyArgProGlyGlyProTrpGlySerProSer  931

Qy   2383 GCTGGCGCCCTCTGGCTCCCCCCA----------------CGGGGCCCTAGAGGGG  2418
          |||
Db    932 SerGlyProSerSerProGluSerSerGluAspSerGlyTyrArgSerSerSerPro  951

Qy   2419 CTACGGCTG----CCCCCCATGCCATGGAAATGTCCCCCAGAGTCTGAGCCCC  2466
          ||||||||                |||   ||||||||||||||||||||||
Db    952 LeuArgLeuValProPheSerSerProArgProGlyGluProGlyGlyProGlyGlyPro  971

Qy   2467 AGGGTAGTAGATGGGCATTGAAGACGGCTGTGGCTCCGACCACCCCAAG--------  2514
          |||||||||||||||||||||||||||||||||||||||||||||||
Db    972 LeuThrGluAspGly----GluLysSerSerAspThrCysAsnProLeuSerGlyAlaPhe  990

Qy   2557 AGCCCC----TCCCCTGGACACAGAGAGCGCGGCCCTTGCTCACTGTT--------------  2595
          |||||                |||||||||||||||||||||||||
Db    991 SerGlyValSerAsnIlePheSerPheSerArgGlyHisGlnTyrGlnGlu  1010

Qy   2596 -----CCCATGGGCCCCAGGAGGCAAGGAACACACACTGGACAAGGCTTCGGCAG  2649
                    |||||||||||||||||||||||||||||||||||||:::|||||
Db   1011 LeuProArgCysProAlaProThrProSerLeuLeuAsnIleLeuProLeuSerSerProCys  1030

Qy   2650 GCGGTGACGAGAGCTGTCAGAGGCAGGGTG---CTGCAGATGCGGGAAGGACTGCAGTCACTT  2706
          :::                              ||| :::|||||||||||||:::
Db   1031 ArgArgProArgGlyAspValGluGlyArg--------LeuAspAlaLeuGlnArg  1046

Qy   2707 CGCCAGGCGTGTCGCAGCTTGTCCTGGCGCCCCACAGGAGGGTCCGTGCCCTGGGCAGCATCG  2766
          |||||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db   1047 GlnLeuAsnArgGlyLeuThrArgLeuSerLeuAlaAspMetAlaThrValLeuGlnLeuLeu  1066
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US-09-965-830-1_COPY_6_3257 (1-3252) x O35221 (1-1162)

DB:
Query Match:         11
Best Local Similarity:    25.41%
Percent Similarity:       32.78%
Score:                    1547.00
Pred. No.:                5.25e-78
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Alignment Scores:

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SQ   SEQUENCE   1162 AA; 126885 MW; A9455F7F10B61E46 CRC64;
PROSITE; PS50042; CNMP_BINDING_3; 1.
SMART; SM00091; PAS; 1.
SMART; SM00086; PAC; 1.
SMART; SM00100; cNMP; 1.
PRINTS; PR01470; ERGCHANNEL.
Pfam; PF00785; PAC; 1.
Pfam; PF00520; Ion_trans; 1.
Pfam; PF00027; cNMP_binding; 1.
InterPro; IPR000014; PAS_domain.
InterPro; IPR000700; PAS-assoc_C.
InterPro; IPR000700; PAC.
InterPro; IPR001610; PAC.
InterPro; IPR000636; M+channel_nlg.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003967; Erg_channel.
InterPro; IPR000595; cNMP_binding.
MGD; MGI:1341722; Kcnh2.
EMBL; AF012870; AAC53422.1; JOINED.
EMBL; AF012870; AAC53422.1; JOINED.
EMBL; AF012871; AAC53420.1; -.
EMBL; AF012871; AAC53420.1; -.
RT   "Two isoforms of the mouse ether-a-go-go-related gene coassemble to
RT   form channels with properties similar to the rapidly activating
RT   component of the cardiac delayed rectifier K+ current.";
RL   Circ. Res. 81:870-878(1997).
OS   Mus musculus (Mouse).
GN   KCNH2 OR MERG1.
DE   MERG1A (MERG1A').
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
AC   O35221;
ID   O35221          PRELIMINARY;    PRT;   1162 AA.
RESULT 12
O35221
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Sequence alignment (nucleotide/protein):

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Qy   1067 GlnArgGlnMetThrLeuIleProProAlaThrTyrSerAlaValThrThrPro--------- 1083
          |||                                   |||
Db   2767 GGAGAGGGCGGTGCCCAGCCAGACCTCCGGGCTTCTGCAGCGCTTCTGTGTGTGGACACT 2826

Qy   1084 ------GlyProGlyThrSerThrSerLeuLeuProValSerProIleProThr        1101
                ||||||  |||||||  ||||||||
Db   1084 ------GlyProGlyThrSerThrSerLeuLeuProValSerProIleProThr 1101

Db   2827 GGGGCATCCTCCTACTGCCTGCAG--------------------------CCCCA 2856

Qy   1102 LeuThrLeuAspSerLeuSerGlnValSerGlnPheMetAlaPheGluGluLeuProPro 1121
                                                              |||
Db   2857 GCTGGCTCTGCTTCTGAGTGGACTTGGCCCCACCCTGCGTCCCCAGGCTGCCT---CCCCTC 2913

Qy   1122 GlyAlaProGluLeu---------------------ProGlnAspGlyProProArgArgLeu 1135
               |||                           ||||||||||
Db   2914 ATGGCACCCTGGCCCTGGGGTGTCCCCAGGCTCTCAG----------- 2949

Qy   1136 SerLeuProGlyGlnIleuGlyAlaLeuThrSerGln 1147

SEQUENCE FROM N.A.
STRAIN=SV129;
MEDLINE=98012815; PubMed=9351462;
London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,
Gilbert D.J., Jenkins N.A., Satler C.A., Robertson G.A.;
```

```
Qy   1   ATGCGGCCANTGGGGGCGGGGCCGGGGGCCTCCTGGCGCCTCAGAACACACGCTTAG 60
         ||||||                          ::||||||||||  ::|||||||||||
Db   1   MetProValArgAlaArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleLeuArg 20

Qy   61  CGGTTCGACGGCGCACGACGAGTAACTTCGTGCGTGGGCAACGGCCAGGTGGCGGGCTCTTC 120
         ||||::::||  ||  :::||  ||||||||||||::::|||||||||||||||
Db   21  LysPheGluGlyGlnLnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys--- 39

Qy   121 CCCGTGGTCTACTGCTTCTGACTTCGTGTGACCTTCACGGGCTTCTCCCGGGCTGAGGTC 180
         ||||                          |||  |||||||
Db   40  AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59

Qy   181 ATGCAGCGGGGGCGTGTGCCTGCGTCCTTCCTTTATGGGGCCAGACACCAGTGAGCTCGCC 240
         |||                 :::|||||||::::||||||||||||||||||
Db   60  MetGlnArgProCysThrCysAspSerPheLeuHisGlyProArgThrGlnArgArgAlaAla 79

Qy   241 CAACAGATCCGCAAGGCCCTGACGAGCCACACAAGGAGTTCAAGCTGAGCTGATCCTGTAC 300
         ||||                      :::||||||       ::|||       ::||||
Db   80  AlaGlnIleIleAlaGlnIleAlaGluLeuGlyValGluGlyLysValGluIleIleAlaPheTyr 99

Qy   301 CGGAAGAGCGGGCGCTCCCGTTCTGGGTGTCCTGGATGTGATACCCATAAAGAATGAGAA 360
         ||||||   |||              ::||||:::||:::||||||||||
Db   100 ArgLysAspGlySerCysPheLeuCysLeuValAspArgValProValLysAsnGluAsp 119

Qy   361 GGGGAGGTGGCCTCTTCCTA---------GTCTCTCACAAGGACATC---------- 399
         ||||                  |||||||         :::||||||
Db   120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysAspMetValGly 139

Qy   400 ----------ACGGAAACCAAGAACCGAGGGGGGCCCCGACAGATGGAAGGAGAGACAGGT-- 447
         ||||||||||||                                            :::|||
Db   140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerTrpLeuAlaSerGlyArg 159

Qy   447 --------------------------------------------------- 447
Db   160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerSer 179

Qy   447 --------------------------------------------------- 447
Db   180 ValArgThrGlySerMetHisSerAlaGlyAlaProGlyAlaValValAlaAspValAsp 199

Qy   447 --------------------------------------------------- 447
Db   200 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValSerAlaMetAsp 219

Qy   220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProGlySer 239
Db   447 --------------------------------------------------- 447

Qy   240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259
Db   448 --------GGTGGCGGCGCGCCCAATATGGCCGGCCACGATCCAAAGGCTTCAATGCC 495

Qy   260 ProAspProAlaSerGlySerSerLeuAlaArgThrArgSerArgGluSerCysAla 279
Db   496 AACCGGCGCGGGGAGGCGGGGGCC--------GTGCTCTACCACGTGCCGGGCGCACCTGCAG 546

Qy   280 SerValArgArgAlaSerSerAlaAspLeuGluAlaMetArgAlaGlyAlaLeuPro 299
Db   547 AAGCAGCACAAGGTCAANTAANAGAGGGGTGTTGGG 591

Qy   300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319
Db   592 GAGAAACCAAAC--------- 603

Qy   320 SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThr 339
Db   603 --------------------------------------------------- 603

Qy   340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359
Db   603 --------------------------------------------------- 603
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SV129;
RX   MEDLINE=98012815; PubMed=9351462;
RA   London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Satler C.A., Robertson G.A.;

Length: 1162
Matches: 413
Conservative: 144
Mismatches: 352
Indels: 351
Gaps: 31

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Qy   603 -----------------------------------------------------------   603
Db   360 IleIleAlaProLysIleLysGluArgThrHisAsnValThrThrGluLysValThrGlnVal   379

Qy   604 -----------------------------------------------------------   604
Db   380 ---TTGCCTGAGTACAAAGTAGCGGCGCCATCCGGAAGTCGCCC   399

Qy   643 TTCATCCCTGTTGCACTGTGGGCACTGAGAGCCACCTGCAGGTTCATCCTGCTCGCC   702
Db   400 TrpThrIleLeuHisTyrSerProPheLysAlaValAlaValTrpAspTrpLeuIleLeuLeu   419

Qy   703 ACACTCTAGTGGCCATCGTCTGCTACTGTGCCTACAGCCGTGTGTG--------------   744
Db   420 ValIleThrTyrThrAlaValPheThrProTyrSerArgAlaAlaPheLeuLeuLysGluThrGlu   439

Qy   745 -------AGCACAGCACGGAGGACCCCAGTGCCGCCCCAGCGGTGTGACCTG   798
Db   440 AspGlySerGlnAlaProAspCysGlyTyrArgLeuAlaCysSerGlnProLeuAlaValAspLeu   459

Qy   799 GCCGTGGAGGTGCCTCCTTCAATCGACAGCGCGTGGGACGTGGCTTCATCCTGCTCGCC   858
Db   460 IleValAspIleMetPheIleValAspIleLeuAsnPheArgThrThrTyrValAsn   479

Qy   859 AAGTCGGGTCCAGGTGGTTTGCCCCAAAGTCCATTGCCTCCACCACCTGG   918
Db   480 AlaAsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrp   499

Qy   919 TTCCTCCTGGATGTCAATCGACAGCGCGTGCCACATGCCTGCCTTCAAGGTCAAC   978
Db   500 PheLeuLeuAspMetValAlaAlaIleProPheAspSerLeu   513

Qy   979 GTGTACTTCGGGGGCC--------------------   1020
Db   514 ---IlePheGlySerGluGlyLeuIleLeuGlyLeuLeuLysThrAlaArgLeuLeu   532

Qy  1021 CGCCTCCTGCTGCTTCCCCGCCTGGTACTGCCACTACCGCCTGTGGCTGTG   1080
Db   533 ArgLeuValAlaArgValAlaLeuArgLysLeuAspAlaArgGlyTyrSerGluTyrArgValAlaAlaValLeu   552

Qy  1081 ACACTGCTCATGGCCGGTGTTCGGGCCCACTGGGGTCGCCGTCGGTTTTAC   1140
Db   553 PheLeuLeuMetCysThrPheAlaLeuLeuIleAlaHisTrpLeuAlaCysIleErrpTyrTyrAla   572

Qy  1141 ATTGGGCCAGGCGGGAGGATCGAGAGCAGCAATCCGAGCTTGGCTGGCTGCAG   1200
Db   573 IleGlyAsnMetGluGlnProHisMetAspSer   589

Qy  1201 GAGCTGGGCGCCGCGGGACTGGGAGACTCCCTACTACCTGTGGGCCGGAGCCGGAGG   1260
Db   590 AsnLeuGlyAspGlnIleLeuGlyLysProTyr   599

Qy  1261 AACAGTCCGGGCCGAGTGACAACTGCAGCACGAGGCCAACGGAGGGGCTG   1320
Db   600 AsnSerSerGly   603

Qy  1321 GAGCTGCCGGGCGGGCGGGCTTCGGCCTGCCTACATCACCTCCCTACTTCGCCACTC   1380
Db   604 ---LeuGlyLeuProSerIleLysSerTyrValThrAlaLeuTyrPheThrThrPhe   621

Qy  1381 AGCAGGCCTCACCAGGCTGGGCCTTCGGCAACGTGTCCGCCAACACGGACACCGAGAAGATC   1440
Db   622 SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysSerIle   641

Qy  1441 TTCTCCATCTGCACCATGCTCATCGGCGCCCCTGATGCACGGCGTGGCTGTTTGGGAACCTG   1500
Db   642 PheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnVal   661

Qy  1501 ACGGCCATCAATCCAGCGGCAGTGCACCCGCCGCCGCCTTTCTGTAACGACAAGGCGGAC   1560
Db   662 SerAlaIleIleGlnLeuArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArg   681

Qy  1561 CTCGCGGACTACATCCGATCACCACCGTATCCCAAGCCCCTCAAGCACACGGCCATGCTGGAG   1620
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Db   682 ValAlaArgGluPheIleArggPheHisSerGlnIleProAsnProLeuAsnArgGlnArgLeuGluGlu   701
Qy  1621 TACTTCCAGGCCCACCTGGCGTGCGGGGGTTGGTGAACAATGGCATTCCGAACCCGCTGAACCGCCAGCGCC   1680

Db   702 TyrPheGlnHisIleAlaThrTrpSerTyrThrArgAsnGlyIleLeuAspMetAsnAlaValLeuLysGly   721
Qy  1681 CTCCCTCACGAGCGCGCCCGCAGCAGCATGCCCAGCACTGCCACCTGGTCGTCGCAG   1737

Db   722 PheProGluCysSerLeuGlnHisAlaAspIleCysSerLeuHisIleLeuAsnArgSerLeuLeuGlnHis   741
Qy  1738 CTGCCACTGTTGAGGGGTGCCAGCCGCGGCGCCAGCGGCCACTGTCTCGGCCCCTGCGG   1797

Db   742 CysLysProPheArgGlyAlaThrLysGlyCysLeuGluArggGlyLeuAlaLeuAlaMetLysPheLys   761
Qy  1798 CCCGGGCCTTCTGCACGCCCCGGGCGAGTACCTTCATCCACCAAGGCCCATGCCCCTCGCCGACCTC   1857

Db   762 ThrThrHisIleAlaProProGlyLysAspThrLeuValHisIleAlaGlyAspProLeuLeuThrAlaLeu   781
Qy  1858 TACTTTGTGTCGTCTCTGGGCTCCCATGGAGGTGCTCAAGGGTGGCACGGTGCCTGCCTGAC   1917

Db   782 TyrPheIleSerSerArgGlySerIleGluIleIleLeuLeuGluArgGlyValValValAlaAlaIleLeu   801
Qy  1918 GGGAAGGGCGCCATCGATCGGGCTGTGCTTGTGAGCTCGACGTGCCCCGGGGGCGGGGACGGTGTAAAGGCCAAT   1977

Db   802 GlyLysLysAsnAspIleLeuPheGlyLeuProLeuAsnLeuuTyrTyrAlaArgProGlyLysSerAsn   821
Qy  1978 GCCGACGTGAAGGGGCTGACGTACTGCTGGTCCTGCGTGGGCACCGTGCTGCCTGCGTGGCTCC   2037

Db   822 GlyAspValArgGlyAlaLeuLeuThrTyrCysAspLeuHisHisLysIleArgGlyAspAspLeuLeu   841
Qy  2038 GACAGCCTTGCGCGTGCTACCCCGAGTTTGCCGGGCCTTCAGTCGTTGGGCCTTCCGAGGGGAG   2097

Db   842 GluValLeuAspMetThrTyrProGluPheSerAspHisHisTrpSerSerLeu   859
Qy  2098 CTCAGCTACAAACCTG---GGTGCTGGGGGGAGGGCTGCAGCAGGTTG   2139

Db   860 IleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGluLeu   879
Qy  2140 GACACACAGTCTCCCTGAGCGCGACGACAAATACCCTTATGTCACGGGGAGGAAGGAGACA   2199

Db   880 GluSerGlyPheAsnArgGlnAsnArgLysLeuSerPheArgArgArgThrArgLys   899
Qy  2200 GATGGGAGCAGGGGCCCCACGGTCTCCCCAGCCTGATGACCCCTCCCAGCCCCCTG   2259

Db   900 AspThrGluGln   903
Qy  2260 CTGTCCCCTGGCTGCGCACCTCTCATCCTACCCACGCTGCCAAGCTGCTATCCCCACGTCGGAACA   2319

Db   904 ---ProGlyGluValSerAlaLeuGlyGln---   917
Qy  2320 GCACCCCGGCGCTCGTCTAGGTGGGGAGAGGGGAGGGGGGGCTTTGAAGGCT   2379

Db   918 GlyProGlyProSerCys---   935
Qy  2380 GAGGCTGGGCCCCTGTCCCCA---   2415

Db   936 SerSerGlyProSerSerGly   955
Qy  2416 GGGCTACGGCCTGCCCCCATGGAATGTGCCCCGAGCCCCAGGGTAGTA   2475

Db   956 ProLeuArgGluValProPheSerSerProArgProGlyGlyGlu   975
Qy  2476 GATGGCCATTGAAGAGACGGCGTGGCCGTGGCTCGGACCAGCCCAAG---   2514

Db   976 ProLeuThrGluAspGlyLysSerAspPhrCysAsnProLeuSerGlyValAlaPheSer   995
Qy  2515 ---TTCTCTTTC---   2541

Db   996 GlyValSerAsnIlePheSerProPheArgProGlyAspSerSerArgGlyGlnTyrGlnGluLeu   1015
Qy  2542 CCGGAATGTAGCAGCAGCCCCTCCCTGGACCAGAGAGCGGCTGCTCACTGTTCCC---   2598
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RESULT 13

Q8WNY2
ID   Q8WNY2          PRELIMINARY;   PRT;   1162 AA.
AC   Q8WNY2;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   ERG potassium channel.
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=COLON SMOOTH MUSCLE;
RA   Shoeb F., Malykhina A., Akbarali H.I.;
RT   "Smooth muscle KCNH2 erg potassium channel.";
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF439342, AAL35327.1; -.
DR   InterPro; IPR000595; CNMP_binding.
DR   InterPro; IPR003967; Erg_channel.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; CNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   PRINTS; PR01470; ERGCHANNEL.
DR   SMART; SM00100; CNMP; 1.
DR   SMART; SM00086; PAC; 1.
DR   PROSITE; PS50042; CNMP_BINDING_3; 1.
DR   PROSITE; PS50112; PAC; 1.
DR   PROSITE; PS50113; PAC; 1.
KW   Ionic channel.
SQ   SEQUENCE   1162 AA;   126858 MW;   18699833BD28B6CF CRC64;
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Alignment Scores:

Pred. No.:
Score:                  8.75e-78
Length:                 1543.00          Length:           1162
Percent Similarity:     44.25%           Matches:          416
Best Local Similarity:  32.99%           Conservative:     142
Query Match:            25.34%           Mismatches:       350
DB:                     6                Indels:           353
                                         Gaps:             33

US-09-965-830-1_COPY_6_3257 (1-3252) x Q8WNY2 (1-1162)
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Qy     1 ATGCGGCCATGCGGGGCCGGCTGGCCGTGGCCGTCCTGGCCGCCCTCAGAACACCTTGGGA... 60
         ||||||||          |||||   ::::||| :::||||||||||||||||||||||||
Db     1 MetProValArgProGlyHisValAlaProGlyHisAsnThrPheLeuAspThrIleIleArg 20

Qy    61 CGCTTCGACGGCAGCACGACAGTAACTTCGTGCTGTGGGCAACGCCCAGGTGCGGGGCTCTTC... 120
         ||||||||||||||   ||||   ||| ||||||||||||||||||||||||||||||||
Db    21 LysPheGluGlyGlnSerArgLysPheIleIleIleAlaAsnAlaArgValAlaGluAsnCys -- 39

Qy   121 CCCGTGCTTCTACTTGCTCTGATGGGCTTCTTGACCTCACGGGGCTTCTCCCGGGTCGAGGTC 180
         ||||||||||||||||   |||   |||||||||||||||||||||||||||||||||
Db    40 AlaValIleTyrCysAsnAspGlyProSerGlyGlyTyrSerArgAlaGluVal 59

Qy   181 ATGCAGCGGGGCGGTGTGCCGGTCCTCCTTTCCTTTATGGGCCCAGAACACCAGGTGCTCCGC 240
         |||||||||||||   |||   |||||||||||||||||||||||||||||||||||
Db    60 MetGlnArgProCysThrCysAspAspPheIleIleIleAlaSerArgArgAlaAla 79

Qy   241 CAACAGGATCCGCAAGGCCCTGGACGAGCACAAGGAGTTCAAGGCTGAGGTGGATCCGTAC 300
         ||||||||||||||||   :::||| ||||||||||||||||||||||||||||
Db    80 AlaGlnHisIleAlaGlnAlaLeuLeuLeuGlyLysAlaGluGlyLysAlaSerPheGluTyr 99

Qy   301 CGGAAGAGCGGGGCTCCCGTTCGTGGTGTCTCCTGGATGTGTACCCATAAAGATTGAGAA 360
         ||||||||||||||   :::|||   ||||||||||||||||||||||||||||||
Db   100 ArgLysAspGlySerCysPheLeuCysLeuValGlyValProValLysProGlyAspGlu 119

Qy   361 GGGGAGGTGGCTCTCTTC--------CTAGTCTCTCACAAGGACATC------- 399
         |||  |||   :::|||                 |||||||::::
Db   120 GlyAlaValIleMetThrPheValLeuAsnPheGluValLysAspMetValGly 139

Qy   400 ---------AGCGAAACCAAGAACCGAGGGGGCCCCGACAGATGGAAGGAGACAGGT--- 447
         |||   |||   |||::||||||||||||||||||||||
Db   140 SerProAlaHisAspThrAsnHisArgGlyProSerTrpLeuAlaSerGlyArg 159

Qy   448 -------GGTGGCGGCGGCCCGCCGGATATGGC------- 468
         :::|||   |||
Db   160 AlaLysThrPheArgGlyLeuLysProAlaLeuLeuLeuThrAlaArgGluSerSer 179

Qy   468 --------AGGGAAGACGGGGCGCTCCCCGTTCGTGGTGTCTCCTGGATGTGTACCCATAAAGATTGAGAA 468
Db   180 ValArgThrGlySerMetArgSerAlaGlyAlaProGlyAlaValValAlaValValAspAlaAsp 199

Qy   496 AACCGGCGGGGCGGAGCCGGGCC 546
         ::: ||||||||||||   :::
Db   220 AsnHisValAlaGlyLeuGlyLeuArgArgAlaLeuValGlyProGlySer 239

Qy   469 ---------CGGGCACGATCCAAAGGCTTCAATGCC 495
         ||| |||
Db   240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259

Qy   260 ProAspAlaSerGlySerCysSerLeuAlaArgThrArgSerArgGluSerCysAla 279
Db   280 SerValArgArgAlaSerSerAlaAspProIleGluAlaMetArgAlaGlyAlaLeuPro 299

Qy   547 AAGCAGCCCAAG------- 591
         |||::::
Db   300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319
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```
Qy    592  GAGAAACCAAAC------------------------------------------------------------  603
                ::|
Db    320  SerThrSerAspSerAspLeuValArgTyrArgThrIleSerLysIleProGlnIleThr            339

Qy    603  ------------------------------------------------------------------------  603

Db    340  LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu            359

Qy    603  ------------------------------------------------------------------------  603

Db    360  IleIleAlaProLysIleLysGluArgThrHisAsnValThrGlnLysValGlnIleVal            379

Qy    604  ------------------------------------TTGCCTGAGTACAAAGTAGCCCGCCATCCGGAAGTCGCC  642
                                              |||||||||||||||||||:::
Db    380  LeuSerLeuGlyAlaAspValLeuProGluGlyTyrLysLeuGlnAlaAlaProArgIleHisArg        399

Qy    643  TTCATCCTGTTGCACTGTGGGCACTGAGAGCCACCTGGGATGGCTTCATCCTGCTGGCC              702
            |||:::|||    |||  ||| |||  |||   |||||  |||||||  ||||||||||||
Db    400  TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuLeu              419

Qy    703  ACACTCTATGTGGCTTGGCTACTGTGCCCTACACAGCGTGTGTG----------------------------  744
            |||  ||| |||||||  ||| ||| |||::::|||||||||
Db    420  ValIleTyrThrAlaValPheThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu            439

Qy    745  ------AGCACAGCGGAGCCCAGTGCCGCCCGCCGGTCGTGACCTG                            798
                  |||  |:: |||||||||||| |||||||||||||||||
Db    440  AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnIleAlaLeuAspLeu                  459

Qy    799  GCCGTGGAGGTCCTCTTCAtCCTTGACATTGTGCTGTACCACANTTCGTGTCC                    858
            |||:::|||||||||||||||||||||||||||||||:::|||||||||||::
Db    460  IleValAspIleMetPheIleValAspIleLeuIleAsnPheArgThrThrTyrValAsn            479

Qy    859  AAGTCGGGCCCAGGTGGTGTTTGCCCCAAAGTCCATTGCCTGTGCTGACCACTGG                  918
            ||||||| ||||||||||| |||
Db    480  AlaAsnGluGluValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrp            499

Qy    919  TTCCTGGCTGATGTCATCGGAGCGCCGTGGGCCGTCCCTGTTTGACCTGTCTGTACATGGTCC          978
            |||||||  ||| |||  |||||||:::|||| ||||||  |||||||||||||||||||||
Db    500  PheLeuIleAspMetValAlaAlaIleAlaProPheAspLeuLeu                          513

Qy    979  GTGTACTTCGGGGCC----------------------------------------                  1020
            |||||||||||||
Db    514  --IlePheGlySerGlyGluGluLeuIleGlyLeuLysGluThrAlaArgLeuLeu                532

Qy    1021 CGCCTCGCTGCGCCTGCTTCCCGCGGTACTCGCAGTACACGCCGTGGTGTG                      1080
            |||::|||    |||  ||||||||||
Db    533  ArgLeuValArgAlaAlaArgLysLeuAspArgTyrSerGluTyrGlyAlaAlaValLeu            552

Qy    1081 ACACTCCTCATGGCCGTGTTCGCCCTGCCCTGCGCGGTCGGCGCCGGTCTGGGTTTTAC              1140
            |||  |||  ||||||||||| |||
Db    553  PheLeuLeuMetCysThrPheAlaLeuIleLeuAlaHisTrpLeuAlaCysIleTrpTyrAla        572

Qy    1141 AATTGGGCAGGCGGGATCGAGAGCAGCAGGAATCCGAGCTGCCTGCTGAGATTGGGCTGCTGCAG        1200
            |||     |||  |||||
Db    573  IleGlyAsnMetGluGlnProHisMetAspSer------His IleGlyTrpLeuHis        589

Qy    1201 GAGCTGGCCCCCGGCCGCCCGCCCGACTGTTCGCCCGACTCCCTACTACTTCGGTGGCCGGAGGGCCCACTGGAGG    1260
            |||
Db    590  AsnLeuGlyAspGlnIleLleGlyLysProCyr                                      599

Qy    1261 AACAGCTTCCGGCCGAGTGACAACTGCAGCAGCAGGAGCCAACGGAGGGGCTG                    1320
            |||||||||
Db    600  AsnSerSerGly------                                                      603

Qy    1321 GAGCTGCTGGGCGCGCCCCGCTGCGCGGCGCTACACACTCCCCTTACTTCGCACTC                  1380
            |||||||
Db    604  ------LeuGlyGlyProSerIleLysAspLysSerTyrValThrAlaLeuTyrPheThrPhe        621

Qy    1381 ACGAGGCCTCACCACGCGTGGGCGGTGGGCAACGTGACCACCGAGAAGATC                      1440
            |||||||||  ||||||||  |||
Db    622  SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle            641

Qy    1441 TTCTCCAACTGCACCATGCTCATCGGCGCCCCCGATGCACGCGGTGGTGTTTGGGAACGTG            1500
            |||||||
Db    642  PheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnVal            661
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```
Db    642  PheSerIleCysValMetLeuIleGlySerLeuMetTyrAlaSerIlePheGlyAsnVal            661
             |||||||||||||:::      |||||||||||||     ::||||||||||
Qy    1501 ACGGCCCATCANCCAGCCANGTACGCCCGGCCGCTTCGTACCACCAGCCGAC                    1560

Db    662  SerAlaIleIleGlnAsnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArg        681
             :::|||    |||   |||||||||||| ||||||||||||||||||||
Qy    1561 CTGCGCGGACTACATCCGCCATCCNCCACCGTATCCCCAAGGCCTCAAGCAGGGGCCATGGGGAG        1620

Db    682  ValArgGluGluHisGlnAlaArgPheHisSerGlnIleProAsnProLeuArgLeuGluGlu        701
             |||     |||||||||:::|||||| |||
Qy    1621 TACTTCCAGGCACCATCGGGGGTGGAGCANATGGCANTGGACNACCACCACCAGCTGCTGCAGAGC        1680

Db    702  TyrPheGlnHisHisAlaArgPheSerTyrThrAsnGlyIleLeuAspMetAsnAlaValAlaLeuLysGlyGly    721
             ||||||||| ||| ||| |||||::: ||| ::::|||
Qy    1681 CTCCCTCGACGAGCCTGCGCGGCAGACAATGCAGCCCATGCACCTGCACAAGGAGGAGGTTGCGCAG    1737

Db    722  PheProGluCysLeuGlnLeuAlaAspIleLeuGluHisLeuAsnArgSerLeuLeuGlnHis        741
             |||||| |||||||||:::|||   :::||||||     |||||||:::||||||
Qy    1738 CTGCCACTGTTTTGAGGCGGGGGCCGCCAGCGGCGCGGCGCCGCGCTCGCGGCACTGTCGCCCCTCGG        1797

Db    742  CysLysProPheArgGlyAlaThrArgLysGlyCysLeuArgAlaLeuAlaMetLysProLys        761
             |||||||||| |||||||   |||   |||||||:::|||:::|||||||||||
Qy    1798 CCCGGCCTTCTGACGCGCGGCGAGTACCTCATTCACCAAGGGCCATGCCCGCCGGCCCTC        1857

Db    762  ThrThrHisHisAlaProProGlyAspThrLeuValHisSerAlaGlyAspLeuLeuHisAla        781
             ||| ||| |||||| ||| |||   |||||||||     |||:::|||||| :::
Qy    1858 TACTTTGTCTGCTCTGGCTCCATGGAGGTGCTGCTCAAGGTGCTGCACCGTCTGCCCATCCTA        1917

Db    782  TyrPheIleSerSerArgGlySerIleGluIleLeuLeuGlyAsnValValTrpLeuAspLeu        801
             |||||||||    |||||||||||||:::|||||||    :::|||:::|||||||
Qy    1918 GGGAAAGGGCGACCTGATGGGCGTGGTTACCCCGAGTTGCCCGGGAGTTGGCCCGGACAGGAAT        1977

Db    802  GlyLysAsnAspIlePheGlyLeuLysGluThrAlaArgProGlyLysSerAsn              821
             ||| ||| ::: |||||| ||| :::||||||
Qy    1978 GCCGACGTGAAAGGGGCTGACGTACTGCCTGCTCCAGTGTGTCTGCGAGCTGCCTGCAC            2037

Db    822  GlyAspValAlaAlaLeuThrArgTyrCysAspLeuHisLysSerIleHisArgAspAspLeu        841
             |||||||:::|||   |||||| |||||||||   ::: |||
Qy    2038 GACAAGCGTTGCGCTGTACCCCGAGTTGCCCGGCGCTTGGCCCTTTCAGGTGCGTTGGCCCTCGAGGGGGAG    2097

Db    842  GluValLeuAspMetTyrProGluPheSerAspHisSerSerLeu-----Glu              859
             :::        |||    ||| ||| |||
Qy    2098 CTCAGCTACAACCTG-------------------------GGTGCTGGGGGAGGCTCTCCAGAGGTG     2139

Db    860  IleThrPheAsnLeuArgAspThrAsnMetIleProGlySerProGlySerAlaGlyLeuLeu        879
             ||||||:::||||||
Qy    2140 GACACAGCTCCCTGAGCGGCGGACAATACCCTTANGTCACGGCTGGGAGGAGGAGAGACA           2199

Db    880  GluSerGlyPheAsnArgGlnArgGlyLysSerSerPheArgArgArgThrArgLys            899
             |||||||||   ||||||
Qy    2200 GATGGGAGCAGGCCCCACGGGTCCCAGCACCTGACTGAGCCTCCAGCGCCCCCTG                 2259

Db    900  AspThrGluGlnProGlyGluVal-----ArgGlyGlnProTrpProGlySerPro            909
             |||    |||||||
Qy    2260 CTGTCCCCNGGCTGCACCCTCANCCTCAGCTCGCCAAGCTGCNATCCCCACGGTCGGAACA           2319

Db    910  LeuGlyGlnGly-------                                                     917
             |||
Qy    2320 GCACCCCGGCCTCGTCTCTAGGGTGGCGGAGGGCGGCAGGGGCGGCTTGAAGGCT                 2379

Db    918  GlyProGlyProSerCys-----ArgGlyGlnProTrpProGlyGluSerPro            935
             |||||||         |||
Qy    2380 GAGGCTGGCGCCCCTCTGCCCCCCA-------------CGGGCCCTAGAG                      2415

Db    936  SerSerGlyProSerSerProGluSerAspGluGlyProGlyArgSerSer                  955
             |||:::
Qy    2416 GGGGTACGGCGTGGCCCCCCANGCCATGGAAAGTGCCCCAGATCGAAGCCCCAGGGGTAGTA         2475

Db    956  ProLeuArgLeuValProPheSerSerProArgProProGlyAspProGlyGlyGlu            975
             |||||||
Qy    2476 GATGGCANTTGAAGAGCGGCTCTGGGCTCGGACCAGCCCAAG-----                        2514
```

RESULT 14
035219

```
ID   035219      PRELIMINARY;      PRT;   1162 AA.
AC   035219;
DT   01-JAN-1998 (TrEMBLrel. 05, Created)
DT   01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Ether-a-go-go-related protein isoform Mergla.
GN   KCNH2 OR MERG1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98012815; PubMed=9351462;
RA   London B., Trudeau M.C., Newton K.P., Beyer A.K., Copeland N.G.,
RA   Gilbert D.J., Jenkins N.A., Satler C.A., Robertson G.A.;
RT   "Two isoforms of the mouse ether-a-go-go-related gene coassemble to
RT   form channels with properties similar to the rapidly activating
RT   component of the cardiac delayed rectifier K+ current.";
RL   Circ. Res. 81:870-878(1997).
DR   EMBL; AF012668; AAC53418.1; -.
DR   MGD; MGI:1341722; Kcnh2.
DR   InterPro; IPR000595; cNMP_binding.
DR   InterPro; IPR003967; Erg_channel.
DR   InterPro; IPR001622; K+channel_pore.
DR   InterPro; IPR000636; M+channel_nlg.
DR   InterPro; IPR001610; PAC.
DR   InterPro; IPR000700; PAS-assoc_C.
DR   InterPro; IPR000014; PAS_domain.
DR   Pfam; PF00027; cNMP_binding; 1.
DR   Pfam; PF00520; ion_trans; 1.
DR   Pfam; PF00785; PAC; 1.
DR   PRINTS; PR01470; ERGCHANNEL.
DR   SMART; SM00100; cNMP; 1.
DR   SMART; SM00091; PAS; 1.
DR   SMART; SM00086; PAC; 1.
DR   PROSITE; PS50042; CNMP_BINDING_3; 1.
DR   PROSITE; PS50112; PAS; 1.
SQ   SEQUENCE 1162 AA;  126693 MW;  B5B16D5F6DA3DA81 CRC64;
```

Alignment Scores:

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Pred. No.:
Score:                     1539.00
Percent Similarity:        44.29%          Length:        1162
Best Local Similarity:     32.86%          Matches:       414
Query Match:               25.28%          Conservative:  144
                                           Mismatches:    351
DB:                                        Indels:        351
                                           Gaps:          32
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us-09-965-830-1_copy_6_3257 (1-3252) x 035219 (1-1162)

```
Qy      1 ATGCCGGCCATGCGGGGGGGGCTCCCTGGCGCGCTCAGAACACACCTTCCTGGACACCATCGGTACG 60
            |||||   :::||||||||||||:||||||||:|||||||||||||||||||||||||||||||||
Db      1 MetProValArgArgGlyHisValAlaLeuProGlnAsnThrPheLeuAspThrIleIleArg 20

Qy     61 CGCTTCGACGGCACCGCACACGTAACTTCGTCGTCGTGGGCAACCGCCCAGGTGGGGGGGGGCTTC 120
            ::||||||:||||||  :||||||||||||| :::|||||||||:|:||||:||||||||||||||
Db     21 LysPheGluGlyLysGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys-- 39

Qy    121 CCGGTGGTCTACTGCTCTGATGGCTTCGTGTGTGACCTCACGGGCTTCTCCCGGGGTCGAGGTC 180
            :::|||   :::|||||||||||||||:||||||||||||||||||||:::|||||||||||||
Db     40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal 59

Qy    181 ATGCAGCGGGGGCGGCTGTGCCTCGTCCTCTCCTTTATGGGCCCAGAACACCAGTGACTCGTCCGC 240
            |||||||||||||||||:|||||||:::|||||:||||||||||||||||||||||||||||||
Db     60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla 79

Qy    241 CAACAGAATCCCGCAAGGCCCCTGGACGAGCACAAGGAGTTCAAGGCTGAAGCTGAGCGTGATCCGTGTAC 300
            |||||||||:::|||||||||:::|||||||||||||||||||||||||||:::|||||||:::
Db     80 AlaGlnIleLeuAlaGlnIleAlaLeuLeuGlyAlaGluLysLysValGluIleAlaPheTyr 99

Qy    301 CGGAAGAAGCGGGCGGCTCCCGTTCTTGGTGTCTCCTGGGATGGTGATACCCATAAAGAATGAGAAA 360
            |||||||||||||||||:::|||||||||||||||:::|||||||||:::|||||||||||||
Db    100 ArgLysAspGlySerCysPheLeuCysLeuValValProValLysAsnGluAsp 119

Qy    361 GGGGAGGTGGCTCTCTCCTTCCTA--------GTCTCTCACAAGGACATC-- 399
            ||||||||||:::|||||||||||        |||:::||||||||||||
Db    120 GlyAlaValIleMetPheIleLeuAsnPheGluValValMetGluLysCysAspMetValGly 139

Qy    400 --------ACCGAAACCAAGACAACCGAGGGGGGCCCCGACACGATGGAGAGACAGGT-- 447
                    ::::||||||||||||||||||||||||||||||||:::|||||||||
Db    140 SerProAlaHisAspThrAsnHisArgGlyProSerThrTrpLeuAlaSerGlyTyrArg 159

Qy    448 --------GGTGGCCGGCGCCGATATGGC-- 468
                    :::|||||||||||:::
Db    160 AlaLysThrPheArgIleLysLeuLeuProAlaLeuLeuLeuThrAlaArgGluSerSer 179

Qy    468 ValArgThrGlySerMetArgSerAlaGlyAlaProGlyAlaAlaValValValAlaAspValAsp 199
Db    180 

Qy    468 LeuThrProAlaAlaProSerSerGluSerLeuAlaLeuAspGluValSerArgAlaMetAsp 219
Db    200 

Qy    468 AsnHisValAlaAlaGlyLeuGlyProAlaGlyLysGluGluGlnArgArgAlaLeuLeuValGlyProGlySer 239
Db    220 
```

```
Db    976 ProLeuThrArgGluAspGlyGluLysSerAsnProLeuSerGlyAlaPheSer 995
Qy   2515 --------------TTCTCTTTC------------------CGCTGGGCCAGTCTGGC 2541
Db    996 GlyValSerAsnIlePheSerPheTrpGlyAspSerArgGlyAlaArgGlnTyrGlnGluLeu 1015
Qy   2542 CCGGAAATGTAGCAGCAGCCCCTCCCCTGGACCACAGAGAGACGCGGGCCGGCTGCTCACTGTTCCC--- 2598
Db   1016 ProArgCys------ProAlaProAlaProSerLeuLeuAsnIleProLeu 1030
Qy   2599 ----------CATGGGCCACCGAGGCAAGGAAACAGAGACACACTGGAC 2637
Db   1031 SerSerProGlyArgArgSerArgGlyAspValGluSerArg------LeuAsp 1046
Qy   2638 AAGCTTCGGCAGGCGGGTGACAGAGCTGTCAGACAGGTG--CTGCAGAATGCGGGAAGGA 2694
Db   1047 AlaLeuGlnArgGlnLeuAsnArgLeuGluProArgLeuSerAlaAspMetAlaThrVal 1066
Qy   2695 CTGCAGTCACTTCGCCAGGGCGTGTGCACCTGTTCCTGGCGCGCCCCACAGGGAGGGTCCGTGC 2754
Db   1067 LeuGlnLeuLeuGln-ArgGlnMetThrLeu------ 1076
Qy   2755 CCTCGGCGCATCGGGAGGGGGAGAGGGGCCGGCCCAGCCACCTCCGGGCTTCTCGAGCCTCTG 2814
Db   1077 --------------ValProProAlaTyrSerAla-- 1083
Qy   2815 TGTGTGGACACTGGGGGGGGATCCTTCCTACTGCCTCCAGCCCCCAGCTGGCTCTGTTCTTGAGT 2874
Db   1084 -ValThrThrProGlyProGlyProThrSerAlaSerProLeuLeuPro------Va 1100
Qy   2875 GGGACTTGGCCCCCACCCTTCGTCCCGGGGGGGCCTCTCCCCATGGCACCCGCCCTGGGGT 2934
Db   1100 1GlyProValProThrLeuThrLeuAspSerLeuSerGln------Va 1114
Qy   2935 CCCCCAGCGTCTC------AGAGCTCCCCTGGGCCTCGGAGCCCAGAGCTTTCTGGACC 2985
Db   1114 1SerGlnPheValAlaPheGlyValLeuProAlaGly--AlaProGluLeuProGlnAs 1133
Qy   2986 TCCACCTTCAGACTCAGAGCCCCCTGCCTCGCTGGACCCCAGCACACCCCT 3045
Db   1133 pGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyLysAlaPheThrHisSerGlnProLe 1153
Qy   3046 G 3046
Db   1153 u 1153
```

```
Qy    468 ------------------------------------------------------------ 468
Db    240 AlaSerProValAlaSerIleArgGlyProHisProSerProArgAlaGlnSerLeuAsn 259

Qy    469 ------------------------------------------------------------ 468
Db    260 ProAspAlaSerGlySerSerCysSerLeuAlaArgThrArgSerArgGluSerCysAla 279
                                         CGGGCCACGATCAAAGGCTTCAATGCC

Qy    496 AACCGGCGGCCGGAGCCGGGGCC-------GTGCTCTACCACTGTCCGGGACCTGCAG 546
          ||||||||||||||||||||||                ::: |||||||||||||||
Db    280 SerValArgArgValAlaSerSerAlaAspAspSerLeuAlaMetArgAlaGlyAlaLeuPro 299

Qy    547 AAGCAGCCCCAAG---------- GGCAAGCACAAGCTCAATAAGGGCTGTGTTTGGG 591
          ||||||||||||               ::|          |||          ::::
Db    300 ProProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn 319

Qy    592 GAGAAACCAAAC-------------------------------------------- 603
Db    320 SerThrSerAspSerAspSerLeuValArgTyrArgThrIleSerLysIleProGlnIleThr 339

Qy    603 -------------------------------------------------------- 603
Db    340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu 359

Qy    603 -------------------------------------------------------- 603
Db    360 IleIleIleAlaProLysIleLysGluArgThrHisAsnValThrGlyLysValThrGlnVal 379
              TTGCCTGAGTACAAACTAGACGCCGCCATCCGAAGTCGCCC

Qy    604 ------------------------------------------ 642
Db    380 LeuSerLeuGlyAlaAspValLeuProGluTyrGlyLeuGlnAlaProArgIleHisArg 399

Qy    643 TTCATCCTGTTGCACTGTGGGCACTGAGAGCCACCTGGGATNGGCTTCATCCTGCTCGCC 702
          :: ||                     ||:::         |||||||||||||||||
Db    400 TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspTrpLeuIleLeuLeuLeu 419

Qy    703 ACACTCTATGTNGGCGTCTCACTGTGCCCTACAGCGTGTGTG---------------- 744
          ||||||||||||||||||||||
Db    420 ValIleThrTyrThrAlaValPheHisThrProTyrSerAlaAlaPheLeuLeuLysGluThrGlu 439

Qy    745 -----AGCACAGCGACGGGACCCCAGTGCCCCAGCCCCCAGCGTCTGTGACCTG 798
               |||:::            |||||||||||||||||||||||
Db    440 AspGlySerGlnAlaProAspCysGlyTyrAlaCysGlnProLeuThrValValAspLeu 459

Qy    799 GCCGTGGGAGGTGCCTTCACCTTGACAATTGTGCTACACACATTCGTGTCC 858
          ||||||||||||||||||||          :::           ||||||||
Db    460 IleValAspIleMetPheIleValAspIleLeuAsnPheArgThrThrTyrValAsn 479

Qy    859 AAGTCGGGTGCAGGTGGTGTTTGCCCCAAAGTCCATTTGCCCCTACTCCACCACCTGG 918
          ||||||||||||||||||||||||          :::                ||||
Db    480 AlaAsnGlyLeuValValSerHisProGlyArgIleAlaValHisTyrPheLysGlyTrp 499

Qy    919 TTCCTGCTGGATGTCATCCGGACCGCCTTGACCGTGCTACACATGCCTTCAAGGTCAAC 978
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    500 PheLeuLeuAspMetValAlaIleAlaIleProPheAspLeuLeu 513

Qy    979 GTGTACTTCGGGGCC----------------CACTGCTGAAGACGGGTGCGGCCTGCTG 1020
          ||||||||||||||                 ||||||||||||||||||||||||
Db    514 ---IleProGlySerGlyLeuGluLeuGlyLeuLeuLysThrAlaArgLeuLeu 532

Qy   1021 CGGCCTGCTGGGCGCCTGCTTCGCCGGCGGTACGCACGCGCGTGGTCGTG 1080
          |||||||||||||||||||||||||||||||||||||||:::
Db    533 ArgLeuArgValAlaArgGlyLeuAspArgTyrSerGluTyrGlyAlaAlaValLeu 552

Qy   1081 ACACTGCTCATGGCCGGGTGTTCGTGCTCGGGTCGCGCTGCGGTTTTAC 1140
          |||||||||||||||||||||||||||||||||||||||||||
Db    553 PheLeuLeuMetCysThrPheAlaLeuIleAlaHisTrpLeuAlaCysIleTrpTyrAla 572

Qy   1141 ATTGGCCAGCGGGAGGATCGAGCACCGAATCCGAGACTCCCTACTACCTGGTGGGCC 1200
          |||| |||          |||          |||||||||||||||
Db    573 IleGlyAsnMetGluGlnProHisMetAspSer-----HisIleGlyTrpLeuHis 589

Qy   1201 GAGCTGGCCCCGCCGACTGGAGAACTCCCTACTACCTGGTGGGCCGGAGGCCAGCTGGAGGG 1260
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    590 AsnLeuGlyAspGlnIleGlyLysProTyr-------- 599

Db    600 AsnSerSerGly--- 603

Qy   1261 AACAGCACCCGGCCAGAGTGACAACTGCAGCCAGCCGCAACGGGACGGGGGCTG 1320
          ||||||||||||
Db    603 ---------------------- 603

Qy   1321 GAGCTGCTGGGGCCGGGGGCCGGTGCGCAGGCGCCTCACATCACCTCCTCTACTTCCACTC 1380
Db    604 ---LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPhe 621

Qy   1381 AGCAGCGCCACCACGGTGGGCGTTCGGCGACCGCGTCCGGCCAACGGGACCGAGAAGATC 1440
          |||          |||||||||||||||||||||||||||||||||||||||||
Db    622 SerSerLeuThrSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle 641

Qy   1441 TTCTCCATCTGCACCATGGTCATCGGGTCCCTGATGCAGGCGTTCTGGTTTGTTGGGAACGTG 1500
Db    642 PheSerIleCysValMetLeuIleGlySerLeuMetLeuLeuMetTyrAlaSerIleProGlnIle 661

Qy   1501 ACGGCCCATCATCAGCGCCATGCAACCGCAGTACGGCCGCCGCCCGCGTTCTGTACCACAGCCCATGCTGGAC 1560
Db    662 SerAlaIleIleGlnLeuAsnArgLeuTyrSerGlyThrAlaArgTyrHisThrGlnMetLeuArg 681

Qy   1561 CTGGCCGGACTACAATCCAGCCGCANCCACCGTANCCCAAGCCCCTCAAGCCACCATGCTGGAG 1620
Db    682 ValArgGluPheIleArgPheHisGlnIleProAsnProLeuArgGlnArgLeuGluGlu 701

Qy   1621 TACTTCCAGGCCACCTGGAGCGTGGGGAACAATGGCANCGACACCACCAGGTCGCTGGCAGAC 1680
Db    702 TyrPheGlnAlaThrTrpSerValGlyAsnAsnGlyIleAspThrThrSerArg 721

Qy   1681 CTCCCTGACGAGCGTNGGCCAGACATGCACCGCCAGGAGGTTCCTGCAG--- 1737
Db    722 PheProGluCysLeuGlnLeuAlaAspIleLeuCysLeuHisLeuAsnArgSerLeuLeuGlnHis 741

Qy   1738 CTGGCCACTGTTTGAGGGCGCCAGCGCCGCGCGCTGCTCTCTGGCCCTGCG 1797
Db    742 CysLysProPheArgGlyAlaThrLysGlyTyrLeuArgAlaLysAlaMetLysPheLys 761

Qy   1798 CCCGCCTTCTGCACGCCCGGGGGTGAGTGGTACCTCCATCACCAAGGCCGAAGCCGATGCCCTCAGGCCCTC 1857
Db    762 ThrThrHisAlaProGlyAspThrLeuValHisSerLeuProGlyAspLeuThrAlaLeu 781

Qy   1858 TACTTGTGTCTGCTCGCTCCCATGGAGGTCGGCCCAAAGGGTGCCACCGGCCTCCCATCCTA 1917
Db    782 TyrPheLeuSerArgGlySerIleGluIleIleGlyGlyAspValValAlaIleLeu 801

Qy   1918 GGGAAGGGCGACCTGATCGGCTGGTGAGCGGGGAGCAGGTGGTGAAAGGCCAAT 1977
Db    802 GlyLysAsnAspIleProPheGlyGluProLeuAsnLeuTyrAlaArgProGlyLysSerAsn 821

Qy   1978 GCCGGACGTGAAAGGGGGCTGACGTACTACGGCGTCCGCAGTGTCTGGCCTGGCGTGCAC 2037
Db    822 GlyAspValArgAlaLeuThrTyrCysAspLeuHisLysIleHisArgAspAspLeuLeu 841

Qy   2038 GACAGCCTGCGCTGTACCACCGACTTTGCCCCGCGAGTTTGCCCTTCAGTGTCGTTGCCCGAGGGGAG 2097
Db    842 GluValLeuAspMetTyrProGluPheSerAspHisPheTrpSerSerLeu----Glu 859

Qy   2098 CTCAGCTACAACCTG--------GGTGCTGGGGGAGGCTCTGCAGAGGTG 2139
Db    860 IleThrProPheAsnLeuArgAspThrAsnMetIleProGlySerProSerAlaGluLeu 879

Qy   2140 GACACCAGCTNCCCTGAGCGGCGACAAATACCCTATGTCCACGCTGGAGAGGACA 2199
Db    880 GluSerGlyPheAsnArgGlnArgLysArgLysLeuSerPheArgArgThrAspLys 899

Qy   2200 GATGGGGAGCAGCAGGGCCCCACGGGTCTCCCCAGCGCCCCAGCTGATGAGCCCTTCCAGCCCCTG 2259
Db    900 AspThrGluGln-------------------- 903

Qy   2260 CTGTCCCCTGGCGTGCACCTTCCCTATCCCCAGCTGCGTAATCCCACGTCGAACA 2319
          ||||||                                        |||  |||
```

```
Db    904 ------ProGlyGluValSerAlaLeuGlyGln------GlyProAlaArgVal  917
Qy   2320 GCACCCCGCTCTGGTTCTTAGGTGGTGCCAGAGGGAGGGCCAGGGGCGCAGGGGCCAGGGGCTTGAAGGCT  2379
Db    918 GlyProGlyProSerCys------ArgGlyGlnProGlyGlyProTrpGlySerPro  935
Qy   2380 GAGGCTGGCCCCCGTCGTCTCCCCCA------CGGGCCCTAGAG  2415
Db    936 SerSerGlyProSerSerProGluSerSerGluGluProGlyArgSerSer  955
Qy   2416 GGGCTACGGCTGCCCCCCATGGAANTGTGCCCCAGATCTCAGCCCCCAGGGTAGTA  2475
Db    956 ProLeuArgLeuValProPheSerSerProArgProProGlyGlyGlu  975
Qy   2476 GATGGCANTGAAGACGGCCGTGGCCTCGGACCAGCCCCAG------  2514
Db    976 ProLeuThrGluAspGlyLysSerSerAspThrCysAsnProLeuSerGlyAlaPheSer  995
Qy   2515 ------CGCGTGGGCCAGTCTGGC  2541
Db    996 GlyValSerAsnIlePheSerThrTrpGlyAsnSerArgGlyArgGlnTyrGlnGluLeu  1015
Qy   2542 CCGGAATGTAGCACAGCCCCTCCCCTGGACAGAGAGCGGGGCCTGCTCACTGTTCCC---  2598
Db   1016 ProArgCys------ProAlaProAlaProSerLeuLeuLeuLeuAsnIleProLeu  1030
Qy   2599 ------CANGGGCCCAGCCAGGCAANGGAACACACACACTGGAC  2637
Db   1031 SerSerProGlyArgArgSerArgGlyAspValGluSerArg------LeuAsp  1046
Qy   2638 AAGCTTCGGCACCAGGCGGTGACAGAGACTGTCAGAGCAGGTG---CTGCAGANTGCGGGGAAGGA  2694
Db   1047 AlaLeuGlnLeuAsnArgLeuGluThrArgLeuSerAlaAspMetAlaThrVal  1066
Qy   2695 CTGCAGTCACTCGCCAGGCTGTGTGCAGTTGTCCTGGGCGCCCCACAGGGAGGGTCCGTGC  2754
Db   1067 LeuGlnLeuLeuGln------ArgGlnMetThrLeu  1076
Qy   2755 CCTCGGACGGCCATCGGAGAGGGCGGCCGTGACCAGCACCTCCGGGGCTTCTGCAGCCTCTG  2814
Db   1077 ------ValProProAlaTyrSerAla  1083
Qy   2815 TGTGTGGGACACTGGGGCATCCTCTACTGCCTCGAGCCCCCCAGTGGCTTGCTGTGCTTGAGT  2874
Db   1084 -ValThrThrProGlyProThrSerAlaSerProLeuLeuPro------Va  1100
Qy   2875 GGGACTTGGGCCCCCACCCCTCGTCTCCCCCCCCCATGGCCACCCTGGGGGT  2934
Db   1100 lGlyProValProThrLeuThrLeuAspProSerLeuSerGln------Va  1114
Qy   2935 CCCCCAG------CGTCTCAGAGCTCCCCCTGGCCTCGAGCACCAGCTTTCTGACCTCC  2988
Db   1114 lSerGlnPheValAlaPheGluGlnLeuProAlaLeuGlyAlaProGluLeuProGlyLeuAspGl  1134
Qy   2989 ACCTCAGACTCAGAGCCCCCTGCCTCAGAGACTCTGCCTCTCAGCCCAGCACCCCTG  3046
Db   1134 yProThrArgArgLeuSerLeuProGlyGlnLeuGlyAlaLeuLeuThrSerGlnProLeu  1153
```

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Alignment Scores:
Pred. No.:                         Length:        1163
Score:               1537.50       Matches:        412
Percent Similarity:  44.09%        Conservative:   144
Percent Identity:    32.67%        Mismatches:     353
Best Local Similarity: 25.25%      Indels:         352
Query Match:         11            Gaps:            31
DB:                  11
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US-09-965-830-1_COPY_6_3257 (1-3252) x O08962 (1-1163)

Qy    1 ATGCCGGCCATGCGGGGGCGGCGCCTCCTGGCGGCCCTCAGAACACCTTCCTGGGACACCATCGGCTACG  60
        |||||           |  ||:|::||||  ||||  | ||  |||| |||||
Db    1 MetProValArgArgGlyHisValAlaProGlnAsnThrPheLeuAspThrIleIleArg  20

Qy   61 CGCTTGCACGGCCACGGCACAGTRAACTTCGGTGTTGGGGAACGCCCAGGTGGCGGGGGCTCTTC  120
        ::||:||:|||:|||           |||   |||:|||  ||| | |||::
Db   21 LysPheGluGlnSerArgLysPheIleIleAlaAsnAlaArgValGluAsnCys---  39

Qy  121 CCCGTGGTCTACTGCCTCTCGATGGCTTCTGTGACCTACACGGGCGTTCTCCCGGGCTGAGGTC  180
        |||:|||    |  ||| ||  ||  | |||:|||||
Db   40 AlaValIleTyrCysAsnAspGlyPheCysGluLeuCysGlyTyrSerArgAlaGluVal  59

Qy  181 ATGCAGCGGGGGCGTGTGCCTGCTGCCTCCTTTANTGGGGCCAGACACCAGTGAGCTGTCCGC  240
        ||||||     |  || |  |:::||||  ::||:|||||||
Db   60 MetGlnArgProCysThrCysAspPheLeuHisGlyProArgThrGlnArgArgAlaAla  79

Qy  241 CAACAGATNCCGCCAAGGCCCTGGACGACGAGCACCAAGGAGTTCAAGGCTGACCTGTAC  300
        |||   |  |  ||||||||   |||:|||
Db   80 AlaGlnIleLeuAlaLeuLeuGlyAlaGluGluArgLysValGlyIleGluAlaPheTyr  99

Qy  301 CGGAAGACGGGCGGCTCCGTTCTTGTGCTGTCTTGCTGTCATACCCATAAAAGATGAGAAA  360
        |||||||||||||    |||||||:||||||||||     ::||
Db  100 ArgLysAspGlySerCysPheLeuCysLeuValAspValProValLysAsnGluAsp  119

Qy  361 GGGGAGGTGGCTCTCTTCCTA------GTCTCTCACAAGGACATC------  399
        ||| | |||       |||:||::                 ||||||:::
Db  120 GlyAlaValIleMetPheIleLeuAsnPheGluValMetGluLysSerAspMetValGly  139

Qy  400 ------AGGGAAAACCAAGAACCGAGGGGGCCCCGACAGGATAGGAGGAGGAGACAGGT--  447
        :::||  |||||||   || | ||     ::||| ::||
Db  140 SerProAlaHisAspThrAsnHisArgGlyProSerThrSerGlyProSerGlyArg  159

Qy  447 ------  447
Db  160 AlaLysThrPheArgLeuLysLeuProAlaLeuLeuAlaLeuThrAlaArgGluSerPro  179

Qy  447 ------  447
Db  180 MetArgThrGlySerThrGlySerProGlyAlaProGlyAlaValValValAspValAsp  199
```

```
Qy    447 ------                                                                                    447
Db    200 LeuThrProAlaAlaProSerSerGluSerLeuLeuAlaLeuAspGluValSerAlaAlaMetAsp                         219

Qy    447 ------                                                                                    447
Db    220 AsnHisValAlaGlyLeuGlyProAlaGluGluArgArgAlaLeuValGlyProAlaSer                               239

Qy    447 ------                                                                                    447
Db    240 AlaSerProValAlaSerIleProGlyProHisProSerProArgProArgAlaGlnSerLeuAsn                         259

Qy    447 ------                                                                                    447
Db    260 ProAspAlaSerGlySerSerCysSerLeuAlaAlaArgThrArgSerArgGluSerCysAla                            279

Qy    496 AACGGCGGCGGGGAGCCGGGCC------ ... GTGCTCTACCACCTGTCCGGCACTGCAG                                546
          |||||||||||||||||||||         :::      |||||||||||||||||        |||
Db    280 SerValAlaArgArgAlaSerAlaAspAspIleGluAlaAlaMetArgAlaGlyAlaAlaLeuPro                        299

Qy    547 AAGCAGGCCAAG-------- ... GGCAAGCACACAAGCTCAATAAGGGGGTTGTTGGG                                591
          :::||||                    |||:::    |||||||||
Db    300 LeuProProArgHisAlaSerThrGlyAlaMetHisProLeuArgSerGlyLeuLeuAsn                               319

Qy    592 GAGAAACCAAAC-------                                                                        603
          :::
Db    320 SerThrSerAspSerAspLeuValArgThrTyrArgThrIleSerLysIleProGlnIleIleThr                        339

Qy    603 ------                                                                                    603
Db    340 LeuAsnPheValAspLeuLysGlyAspProPheLeuAlaSerProThrSerAspArgGlu                               359

Qy    603 ------                                                                                    603
Db    360 IleIleLeuAlaProLysIleGluArgThrHisAsnValThrGluLysValThrGlnVal                               379

Qy    604 ------ ... TTGCCTGAGTACAAAAGTAGCCCCATCCGGAAGTCGCCC                                         642
                    ||||||||||        ||||||||||
Db    380 LeuSerLeuGlyAlaAspValLeuProGluTyrLysLeuGlnIleAlaProArgIleHisArg                            399

Qy    643 TTCATCCCTGTTGCACTGTGGGGCACTGGAGAGCCACCTGGAATGTCGTCATCCTGCTCGGC                            702
          |||:::||||||||||||        |||||||||||||        |||||||
Db    400 TrpThrIleLeuHisTyrSerProPheLysAlaValTrpAspProIleLeuLeuLeuLeu                               419

Qy    703 ACACTCTATGTGGCTGTGACTGTGCCCTTACAGCGTGTGTG----------                                       744
          ::: ||||
Db    420 ValIleTyrThrAlaValPheThrProTyrSerAlaAlaAlaPheLeuLeuLysGluThrGlu                            439

Qy    745 ----- AGCACAGCACGGGAGCCCAGTGCCGCGCCCCCCCAGCGTCGTGACCTG                                     798
               ||||||||||        ||||||||||
Db    440 AspGlySerGlnAlaAlaProCysGlyTyrAlaCysGlyGlnProLeuAlaValAlaAspLeu                            459

Qy    799 GCCGTGGAGGTCCTCTTCAATCCTTGACAATTGTCTGAATTTCCGTGACCAATTCGTGTCC                            858
          ||||||||||||||:::        ||||||:::        ||||||
Db    460 LeuValAspIleMetPheIleValAspIleLeuGluAsnPheArgThrThrArgTyrValAsn                            479

Qy    859 AAGTCCGGCCCAGTGGGTGTTTGCCCCAAAGTCCATTGCCTCCACTAGTCACCACCTGG                               918
          ||||||||||:::        ||| :::    ||||||
Db    480 AlaAsnGluValIleValSerHisProGlyArgIleAlaValHisThrPheLysGlyGlyTrp                            499

Qy    919 TTCCTGCTGGGATGTCAATGCAGAGGCCTGCCCCTTTGACCTGCTACAATGCCTTCAAGGTCAAC                         978
          ||||||        ||||||||||
Db    500 PheLeuLeuGluAspMetValAlaAlaIleProPheAspLeuLeu                                             513

Qy    979 GTGTGACTTCGGGGCC                                                                           1020
          |||||||
Db    514 ---IlePheGlySerGlyLeuGluLeuLeuGlyLeuLeuLysThrAlaArgLeuLeu                                  532

Qy    1021 CGGCTGCTGCCGGCCTGCTTCCGGCGGCTACTCGACAGCCGGGTACAGGCGGGTGCTGCTG                            1080
           ||||||        :::|||
Db    533 ArgLeuValAlaArgValAlaLeuAlaLeuArgLysLeuAspProAlaThrYrSerGluTyrGlyLeuAlaAlaValLeu          552

Qy    1081 ACACTGCTCATGGCCGTGTTCGCCCTGCACTGGGTCGCCTGCGTGTCTGGTTTTAC                                 1140
           ||||||||||        :::|||
Db    533 ...                                                                                      552
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Db    553 PheLeuLeuMetCysThrPheAlaLeuLeuHisAlaHisTrpLeuAlaCysSerIleProTyrAla                        572
          |||||||||

Qy    1141 ATTTGGCCGGGGAGGATCGAGAGCAGGATCACGAGATCGGAGACTGCCTGAGAATTGGCTGGCAG                        1200
           |||||||        |||
Db    573 IleGlyTyrGlyAsnMetGluGlnProHisMetAspSer------ HisIleGlyTrpLeuHis                           589

Qy    1201 GAGCTGCGCCCCGCCGACTGGAGACTCCCTACTACTTCGGTGGGCCGGAGGCCAGCCTGCGAGGG                        1260
           ||||||||||        ||||||
Db    590 AsnLeuGlyAspGlnIleIleGlyLysProTyr------                                                   599

Qy    1261 AACACTCCCGGCCAGAGTGACAACTGCAGCAGCAGCAGCGAGGCCAACGGGCGGGGCTG                              1320
           |||||||        |||||||
Db    600 AsnSerSerGly------                                                                        603

Qy    1321 GAGCTGCTGGGCGGCCCGGCCCTGGCTGCGCCCAGGCCCTACAATCACCTCCTTACTTCGGCACTC                      1380
           |||||||||||        ||||||
Db    604 ------ LeuGlyGlyProSerIleLysAspLysTyrValThrAlaLeuTyrPheThrPhe                              621

Qy    1381 AGCAGGCCTCCACCAGCGTGGGGCGTTCGGCTTCGCCAAGTGTCCGCCAACACCGGACACCGGAGAAGATC                  1440
           ||||||||||        ||||||
Db    622 SerSerGlyLeuThrHisSerValGlyPheGlyAsnValSerProAsnThrAsnSerGluLysIle                        641

Qy    1441 TTCTCCATCTGCACCATGCTCATCGGCGGCCCGTTGAGCGCGGCCCTGATCGCCGGGGGTGGTGTTGGGAACGTG             1500
           ||||||||||        ||||||
Db    642 ValAlaGlyLeuPheHisIleGlnIleLeuProAsnProLeuuArgGlnLeuGlu                                   661

Qy    1501 ACGGGCCATCAACACCACGGTGAGTCACCGGCCGCCCGCCGCTTTCTTGTCAGCCACGGGCGAC                        1560
           ||||||||||||:::        |||
Db    662 SerAlaIleIleGlnArgLeuGlyCysLysLeuGluuArgAlaAlaGlyTyrHisThrGlnMetLeuArg                     681

Qy    1561 CTGCGCGACTACATCCGACATCCACCGTATCCCCAAGCCCTACCTCGACACCAGCGACCCCATGCTGGAG               1620
           ||||||||||        |||
Db    682 ValAlaArgGluPheHisGlnIleIleProAsnProLeuArgGlnLeuGlu                                        701

Qy    1621 TACTTCCAGGCGCCACCTGGCGGCGTGAACAATGGCAATGACCGGCCGCCGGCGACAGCTGCTGCAGAGC              1680
           ||||||||||        |||||||
Db    702 TyrPheGlnIleHisAlaIleTrpSerTyrThrAsnGlyIleAspMetAsnAlaValLeuLysGly                        721

Qy    1681 CTCCCTGACGAGCTGCCGCGAGAACATCGCCAACTGCACCTTGCACAACAAGGAGGTCCTGACCTA                      1737
           ||||||||||        |||||||
Db    722 PheProGluCysSerGlnIleLysAlaAspIleLeuLysLeuHisSerLeuuAsnArgSerLeuLeuLeuHis                   741

Qy    1738 CTGGCCACTGTTTGAGGCGGCCAGCCGCGGCGGTGCCTGCGGCGGCGGGCACTGTGTCTCTGCCCTGCGG             1797
           |||:::
Db    742 CysLysProPheArgGlyLysAlaThrLysGlyCysLysLeuuArgAlaAlaMetLeuysPheLys                          761

Qy    1798 CCCGGCCTTCTTGCCACGCGCGGAGTGACCTCATCCACCACGGACCGGATGCCCTGCAGGCCCTC                      1857
           ||||||||||        ||||||
Db    762 ThrThrHisIleAlaProGlyAspThrLeuValHisAlaGlyAspLeuGlyuLeuThrAlaLeu                            781

Qy    1858 TACTTTGTCTGCCTCTGGCCTCCATGAGGTGCTCAAGGGGTGGCACCGTGCTGCCACCCTA                          1917
           |||||||        :::|||
Db    782 TyrPheIleSerArgGlyLeuIleGluIleLeuGluuArgGlyAspValValAlaIleLeu                              801

Qy    1918 GGGAAGGGCGGCACCTGATCGCGTGTGAGCCTGCCCCGGGGAGCCAGGTGGTGGGAAAAGCCAAT                       1977
           ||||||||||        |||||||
Db    802 GlyLysGlyAsnAspIleIleProGluGlyLysProLeuuAsnLeuuTyrAlaArgProGlyLysSerAsn                     821

Qy    1978 GCCGACGTGAAGGGCGTGGAGGTACTGCCGTGCGTCTCGCAGTGTGTCCTGGCTGTCTGCAC                         2037
           ||||||||||        ||||||
Db    822 GlyAspValArgAlaLeuuThrTyrCysAspSerLeuHisLysIleHisArgAspAspLeuLeu                            841

Qy    2038 GACAGGCCTTCGGCCTGTACCCGGAGTTGCCCGCGCCTTCAGTCGTGGCCTCCGAGGGGAG                           2097
           ||||||||||        |||
Db    842 GluValLeuuAspMetTyrProGlyPheSerAspHisProPheArgProSerSerLeu------ Glu                       859

Qy    2098 CTCAGCTACAACCTG------ GGTGCTGGGGAGGGGAGGCTGCTGGAAGGAGGACA                               2139
           ||||||||||        :::|||
Db    860 IleThrProPheAsnLeuuArgAspThrAsnMetIleProGlyLysSerProSerSerAlaGluuLeu                        879

Qy    2140 GACACCAGCTCCCTGAGCGCGACAATACCCTTAGTCACGCTACGGGAGGAAGGAGACA                             2199
           :::|||
Db    879 ...                                                                                      879
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Db    880  GluSerGlyPheAsnArgGlnArgGlyLysSerPheArgLysArgThrAspLys  899

Qy   2200  GATGGGGAGCAGGGCACCCCACGGTCTCCCAGCCCCAGCCCTGAATGAGCCCCCCTG  2259
           ||| ||||||
Db    900  AspThrGluGln----------------------------------------------  903

Qy   2260  CTGTCCCCTGGGTGCACCTCCTCATCCTCAGCGTGCCAAGCTGTATCCCACGTCGAACA  2319
           ||||||                                     |||||
Db    904  -----------ProGlyGluValSerAlaLeuGlyGln---------GlyProAlaArgVal  917

Qy   2320  GCACCCCGGCCCTCGTCTAGGTGGCCAGAGGGGAGGGGCCAGGGCAGGGGCCTTTGAAGGCT  2379
           |||                                           |||:::||||||||
Db    918  GlyProGlyProSerCys------------ArgGlyGlnProGlyGlyProTrpGlyGluSerPro  935

Qy   2380  GAGGCTGGCCCCCTCTGCTCCCCCA-------------------------CGGGCCCTAGAG  2415
           :::|||||||||:||:||:||||                          |||
Db    936  SerSerGlyProSerSerSerProGluSerSerGlyGluGlyProGlyArgSerSerSer  955

Qy   2416  GGGCTACGGGCTGCCCCCATGCCATGGAATGTGCCCCCAGATCTGAGCCCCAGGGTAGTA  2475
           ||||||
Db    956  ProLeuArgLeuValProPheSerSerProArgProProGlyAspSerProGlyGlyGlu  975

Qy   2476  GATGGCATTGAAGACGGGCTGTGGCCTCGGACCAGCCC-------------------  2511
           ||||||||||
Db    976  ProLeuThrGluAspGlyLeuValSerSerAspThrCysAsnProLeuSerGlyAlaPhe  995

Qy   2512  ----------AAGTTCTCTTTC------------------CGGCTGGGCGCCAGTCT  2538
           ||||||||||                        |||
Db    996  SerGlyValSerAsnIlePheSerPheThrProGlyTyrAspSerArgGlyArgGlnTyrGlnGlu  1015

Qy   2539  GGGCCCGGAATGTAGCAGCAGCCCCTCCCCCCTGGACCAGAGAGCGGGCCTGGCTCACTGTTCCC  2598
           :::|||||||||                         ||||||        |||||
Db   1016  LeuProArgCys----------ProAlaProAlaProSerLeuLeuAsnIlePro  1030

Qy   2599  -------------------CATGGGCCCGAGGCAAGGAACACAGAACACTG  2634
           |||:::||||||
Db   1031  LeuSerSerProGlyArgArgSerArgGlyAspValGluSerArg--------------------Leu  1046

Qy   2635  GACAAGCTTCGGCAGGCGGTGACAGAGCTGTCAGAGCAGGTG--CTGCAGATGCGGGAA  2691
           |||||:|::|                         :::          |||
Db   1047  AspAlaLeuGlnArgGlnLeuAsnArgGluThrArgLeuSerAlaAspMetAlaThr  1066

Qy   2692  GGACTGCAGTCACTTCGCCAGGCTGTGCAGCTTGTCCTGGCGCCCCACAGGGAGGGTCCG  2751
           |||||||||
Db   1067  ValLeuGlnLeuLeuGln-ArgGlnMetThrLeu--------------------------  1077

Qy   2752  TGCCCTCGGGCATCGGGGAGAGGGGCCGTGCCCAGCCAGCACCTCCGGGCGCTTCTCCAGCCGT  2811
           ||||||||||
Db   1078  --------------------------ValProProAlaTyrSerAla--  1084

Qy   2812  CTGTGTGTGGACACTGGGGGCAATCCTCCTACTGCCCTGCAGCCCCCGGCTGGCTCTGTCTTG  2871
           |||||||||||||:::|||
Db   1085  -----ValThrThrProGlyProGlyProThrSerProLeuLeuPro------  1100

Qy   2872  AGTGGGACTTGGCCCCACCCTCGTCCGGGGGCCCCTCCCCTCATGGCACCCTGCCCCTGG  2931
           ||||||||  |||
Db   1101  -ValGlyProValProThrLeuThrLeuAspSerLeuSerGln-----------------  1114

Qy   2932  GGTCCCCCAG------CGTCTCAGAGCTCCCCCTGGCCTTCGAGCCACACTTTCTGGACC  2985
           |||||||||       |||:::||||:::|||
Db   1115  -ValSerGlnPheValAlaPheGluGluLeuProAlaGlyIyAlaProGluLeuProGlnAs  1134

Qy   2986  TCCACCTCAGACTCAGAGACCCCCTTGCCTCAGGAGACCTTCTGCTCTGACCCCAGCACCCCT  3045
           |||||||:::                           |||||||||::
Db   1134  pGlyProThrArgArgLeuSerLeuProGlyGlnLeuGlyLyAlaLeuThrSerGlnProIle  1154

Qy   3046  G  3046
           |
Db   1154  u  1154
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